

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 14:26:51 ; Search time 167 Seconds
(without alignments)
734.150 Million cell updates/sec

Title: US-09-211-315-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec
5	1685	100.0	317	3	AAY84417	Aay84417 Amino aci
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful
8	1685	100.0	317	5	ABB08134	Abb08134 Human RAN
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN

10	1685	100.0	317	5	ABG31631	Abg31631	Human	RAN
11	1685	100.0	317	5	AAU78285	Aau78285	Human	TRA
12	1685	100.0	317	5	AAO19096	Aao19096	C neoform	
13	1685	100.0	317	5	ADR29336	Adr29336	Human	RAN
14	1685	100.0	317	6	ABP55108	Abp55108	Human	ost
15	1685	100.0	317	6	AAE34364	Aae34364	Human	rec
16	1685	100.0	317	6	ABR42314	Abr42314	Human	RAN
17	1685	100.0	317	7	ADB16988	Adb16988	Human	rec
18	1685	100.0	317	7	ADC35204	Adc35204	Human	TNF
19	1685	100.0	317	7	ADC73002	Adc73002	Human	RAN
20	1685	100.0	317	7	ADC78268	Adc78268	Human	RAN
21	1685	100.0	317	7	ABW02277	Abw02277	Human	RAN
22	1685	100.0	317	7	ADG46723	Adg46723	Human	RAN
23	1685	100.0	317	7	ADJ82112	Adj82112	Protein f	
24	1685	100.0	317	8	ADM96241	Adm96241	Human	rec
25	1685	100.0	317	8	ADT08155	Adt08155	Human	RAN
26	1677	99.5	317	2	AAW83018	Aaw83018	Osteoclas	
27	1424.5	84.5	316	5	ADR29338	Adr29338	Mouse	RAN
28	1424.5	84.5	316	8	ADT08153	Adt08153	Murine	RA
29	1422	84.4	270	7	ADJ82113	Adj82113	Protein f	
30	1417.5	84.1	316	2	AAW83017	Aaw83017	Osteoclas	
31	1417.5	84.1	316	2	AAW83194	Aaw83194	Human	ost
32	1417.5	84.1	316	2	AAW59654	Aaw59654	Amino aci	
33	1417.5	84.1	316	2	AAY17874	Aay17874	Murine	TR
34	1417.5	84.1	316	3	AAY91024	Aay91024	Mouse	OBM
35	1417.5	84.1	316	3	AAY84418	Aay84418	Amino aci	
36	1417.5	84.1	316	3	AAY84419	Aay84419	Amino aci	
37	1417.5	84.1	316	5	AAU78289	Aau78289	Mouse	TRA
38	1417.5	84.1	316	6	ABR42071	Abr42071	Human	RAN
39	1417.5	84.1	316	6	ABB99477	Abb99477	Amino aci	
40	1417.5	84.1	316	6	ABU08463	Abu08463	Amino aci	
41	1417.5	84.1	316	6	ABR55560	Abr55560	Amino aci	
42	1396.5	82.9	318	4	AAB82092	Aab82092	Rat	osteo
43	1326.5	78.7	294	2	AAW69956	Aaw69956	NF-kB	rec
44	1326.5	78.7	294	2	AAW68292	Aaw68292	NF-kB	rec
45	1326.5	78.7	294	2	AAE08737	Aae08737	Murine	re

ALIGNMENTS

RESULT 1

AAW83195

ID AAW83195 standard; protein; 317 AA.

XX

AC AAW83195;

XX

DT 11-FEB-1999 (first entry)

XX

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.

XX

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;

KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;

KW hypercalcaemia; osteoclast differentiation and activation receptor;

KW Paget's disease.

XX

OS Homo sapiens.

XX
 PN WO9846751-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-US007584.
 XX
 PR 16-APR-1997; 97US-00842842.
 PR 23-JUN-1997; 97US-00880855.
 PR 30-MAR-1998; 98US-00052521.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ;
 XX
 DR WPI; 1998-594578/50.
 DR N-PSDB; AAV70285.
 XX
 PT Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g.
 PT treating bone diseases by modulating osteoclast differentiation and for
 PT diagnosis.
 XX
 PS Claim 19; Fig 4; 47pp; English.
 XX
 CC The present sequence is human osteoprotegerin (OPG) binding protein. Host
 CC cells transfected with vectors containing nucleic acid molecules encoding
 CC OPG binding protein are used to produce recombinant OPG binding protein.
 CC OPG binding protein is used in binding assays to determine osteoprotegrin
 CC (OG) in biological samples; to screen for specific binding agents
 CC (particularly agonists and antagonists, including intracellular proteins)
 CC ; to raise Ab (useful in immunoassays for detection of OPG binding
 CC protein) and to identify compounds that modulate binding of OPG binding
 CC protein to osteoclast differentiation and activation receptor (ODAR). The
 CC nucleic acid molecule encoding OPG binding protein can be used to detect
 CC OPG binding protein-encoding sequences, e.g. screening for related
 CC sequences, also to produce transgenic animal models, while complementary
 CC sequences are used for antisense regulation of OPG binding protein
 CC expression. Modulators of OPG binding protein, particularly soluble forms
 CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,
 CC e.g. osteoporosis, bone loss caused by arthritis or metastases,
 CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,
 CC loosening of prostheses, optionally in combination with agents that
 CC promote bone growth
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.5e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
 |||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

AAW69957

ID AAW69957 standard; protein; 317 AA.

XX

AC AAW69957;

XX

DT 08-OCT-1998 (first entry)

XX

DE NF-kB receptor activator RANK ligand (RANKL).

XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis; RANKL;

KW RANK ligand; tumour necrosis factor; TNF.

XX

OS Homo sapiens.

XX

PN WO9828426-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US023775.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Anderson DM, Galibert LJ, Maraskovsky E;

XX

DR WPI; 1998-377657/32.

DR N-PSDB; AAV41378.

XX

PT New isolated ligand for receptor activator of NF-kappa B - used to

PT develop products for augmenting an immune response for inhibiting an

PT inflammatory response and for protection of cells.

XX

PS Claim 27; Page 59-60; 80pp; English.

XX


```
DT      08-OCT-1998   (first entry)
XX
DE      NF-kB receptor activator RANK ligand (RANKL).
XX
KW      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW      immune response; inflammatory response; toxic shock; sepsis; RANKL;
KW      RANK ligand; tumour necrosis factor; TNF.
XX
OS      Homo sapiens.
XX
PN      WO9828424-A2.
XX
PD      02-JUL-1998.
XX
PF      22-DEC-1997;    97WO-US023866.
XX
PR      23-DEC-1996;    96US-0059978P.
PR      07-MAR-1997;    97US-00813509.
PR      14-OCT-1997;    97US-0064671P.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR      WPI; 1998-377655/32.
DR      N-PSDB; AAV41372.
XX
PT      New isolated receptor activator of necrosis factor-kappa B - useful for,
PT      e.g. developing products for regulating an immune or inflammatory
PT      response, treating toxic shock or sepsis.
XX
PS      Example 7; Page 59-60; 80pp; English.
XX
CC      This represents a human RANKL, a ligand for the RANK (receptor activator
CC      of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the
CC      tumour necrosis factor (TNF) family. Host cells transformed or
CC      transfected with an expression vector comprising the RANK encoding
CC      nucleic acid can be used to produce recombinant RANK protein. The soluble
CC      RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC      expressing membrane-associated RANK with a soluble RANK which binds to
CC      RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC      used for regulating an immune or inflammatory response. Inhibition of NF-
CC      kB by RANK antagonists may be useful in ameliorating negative effects of
CC      an inflammatory response that result from triggering of RANK, e.g. in
CC      treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC      inflammatory reactions. They can also be used in adjunct therapy for
CC      disease characterised by neoplastic cells that express RANK. The products
CC      can also be used for detection and drug screening
XX
SQ      Sequence 317 AA;

Query Match          100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPAAASRSMFVALLGLGLGV 60
        |||||||
```

Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180
 |||

Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||

Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
 |||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 4

AAE08738

ID AAE08738 standard; protein; 317 AA.

XX

AC AAE08738;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human receptor activator of NF kappaB ligand (RANKL) protein.

XX

KW Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF;

KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;

KW immune response; inflammatory response; graft-versus-host reaction;

KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;

KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX

OS Homo sapiens.

XX

PN US6271349-B1.

XX

PD 07-AUG-2001.

XX

PF 17-DEC-1998; 98US-00215649.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 23-DEC-1996; 96US-00772330.

PR 07-MAR-1997; 97US-0077181P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Dougall WC, Galibert L;

Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240
 |||

Db 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
 |||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

AA Y84417

ID AAY84417 standard; protein; 317 AA.

XX

AC AAY84417;

XX

DT 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

KW tumour necrosis factor receptor; type II transmembrane protein;

KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;

KW osteoporosis; bone resorption.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	49. .69
----	--------	---------

FT		/note= "transmembrane region"
----	--	-------------------------------

FT	Domain	70. .157
----	--------	----------

FT		/note= "extracellular stalk domain"
----	--	-------------------------------------

FT	Region	158. .317
----	--------	-----------

FT		/note= "active ligand moiety"
----	--	-------------------------------

XX

PN WO200015807-A1.

XX

PD 23-MAR-2000.

XX

PF 13-SEP-1999; 99WO-DK000481.

XX

PR 15-SEP-1998; 98DK-00001164.

PR 02-OCT-1998; 98US-0102896P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Halkier T, Haaning J;

XX

DR WPI; 2000-271444/23.

DR N-PSDB; AAZ99964.

XX

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to

PT treat, prevent and ameliorate osteoporosis.

XX

PS Claim 19; Page 78-79; 110pp; English.

XX

CC The present sequence represents a human osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of OPGL
CC activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 3; Length 317;

Best Local Similarity 100.0%; Pred. No. 6.5e-154;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          |||
Db    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKT SIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db    241 YVTKT SIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 6

AAE04426

ID AAE04426 standard; protein; 317 AA.

XX

AC AAE04426;

XX

DT 04-SEP-2001 (first entry)

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
 |||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 7

AAE01993

ID AAE01993 standard; protein; 317 AA.

XX

AC AAE01993;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human full-length RANKL (receptor activator of NF-kappaB ligand).

XX

KW Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.

XX

OS Homo sapiens.

XX

PN WO200136637-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-US031459.

XX

PR 17-NOV-1999; 99US-00442029.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Anderson DM, Hughes AE;

XX

DR WPI; 2001-329222/34.

DR N-PSDB; AAD05904.

XX

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 PT treatment of Pagets disease and Familial Expansile Osteolysis (FEO).

XX
PS Disclosure; Page 76-77; 96pp; English.

XX
CC The present invention relates to a novel receptor, referred to as RANK
CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a Type I
CC transmembrane protein that interacts with TNF receptor-associated factors
CC (TRAFs). Triggering of RANK by overexpression or co-expression of RANK
CC and membrane bound RANK ligand (RANKL) results in upregulation of the
CC transcription factor NF-kappaB, a ubiquitous transcription factor that is
CC most extensively utilised in cells of the immune system. Inhibition of Nf
CC -kappaB by RANK antagonists is useful in ameliorating negative effects of
CC inflammatory reactions, and the effects of excess bone resorption. The
CC RANK DNAs, proteins and their analogues are useful for the preparation of
CC pharmaceutical compositions, for infecting target cells for use in gene
CC therapy applications in diagnosing diseases associated with RANK, and as
CC targets for use in screening assays. They may be used in the treatment or
CC diagnosis of immune system dysfunction. The present invention also
CC encompasses gene therapy methods to correct gene-activating mutations,
CC associated with e.g. familial expansile osteolysis (FEO) and early onset
CC Paget's disease of bone (EP). The present amino acid sequence is full-
CC length human RANKL (huRANKL) protein. The RANKL gene is located in
CC chromosome 13q14

XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
|
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLMV 240
|
Db 181 KVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300
|
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
|
Db 301 PDQDATYFGAFKVRDID 317

RESULT 8
ABB08134

ID ABB08134 standard; protein; 317 AA.
XX
AC ABB08134;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human RANKL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; RANKL.
XX
OS Homo sapiens.
XX
PN WO200236141-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US044834.
XX
PR 02-NOV-2000; 2000US-0245721P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas EK;
XX
DR WPI; 2002-500114/53.
XX
PT Treating an individual suffering from infection, e.g. inflammation,
PT chickenpox or AIDS, by administering a combination of dendritic cell
PT mobilization factor or maturation agent, T cell enhancing factor and
PT antigen-specific T cells.
XX
PS Disclosure; Page 42-43; 43pp; English.
XX
CC The invention relates to treating an individual at risk for or suffering
CC from infection with a pathogenic or opportunistic organism. The method
CC involves administering a combination of two to five agents comprising:
CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
CC or (e) activated, antigen-specific T cells. The methods are useful for
CC treating an individual at risk for or suffering from infection with a
CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
CC T. cruzi, which causes Chaga's disease). The methods are especially
CC useful for treating an individual suffering from immunosuppression by
CC enhancing a lymphocyte-mediated immune response. In particular, the
CC method is useful for treating inflammations, chickenpox, oral or genital
CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
CC cell leukemia or T cell lymphoma. The activated antigen-presenting
CC dendritic cells are useful as a vaccine adjuvant. The present sequence
CC represents a human RANKL polypeptide fragment
XX
SQ Sequence 317 AA;

Query Match

100.0%; Score 1685; DB 5; Length 317;

Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 9

AAE26103

ID AAE26103 standard; protein; 317 AA.

XX

AC AAE26103;

XX

DT 14-NOV-2002 (first entry)

XX

DE Human RANK ligand (RANKL) protein.

XX

KW Human; RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;
KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;
KW tumour necrosis factor receptor-associated factor; immunosuppressive;
KW antibacterial; antiinflammatory; chromosome 13.

XX

OS Homo sapiens.

XX

PN US2002086827-A1.

XX

PD 04-JUL-2002.

XX

PF 30-MAY-2001; 2001US-00871291.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-0077181P.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

PR 17-DEC-1999; 99US-00466496.

PR 24-MAY-2000; 2000US-00577800.

XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM;
XX
DR WPI; 2002-642254/69.
DR N-PSDB; AAD43213.
XX
PT A novel RANK (receptor activator of nuclear factor-kappaB (NF-kB))
PT polypeptide, useful for inhibiting activation of NF-kB and for regulating
PT an immune or inflammatory response in an individual.
XX
PS Example 15; Page 35; 49pp; English.
XX
CC The invention relates to novel RANK (receptor activator of nuclear factor
CC -kappaB (NF-kB)) proteins and polynucleotides encoding them. Sequences of
CC the invention are useful for inhibiting activation of NF-kappaB. They are
CC useful for regulating an immune or inflammatory response in an individual
CC at risk for an immune or inflammatory response. Inhibition of NF-kappaB
CC by RANK antagonists is useful in ameliorating negative effects of an
CC inflammatory response that results from triggering of RANK, for e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions or acute
CC inflammatory reactions. Soluble RANK is useful as an adjunct therapy for
CC diseases characterised by neoplastic cells that express RANK. Soluble
CC forms of the receptor are useful in vitro to screen for agonists or
CC antagonists of RANK activity. The cytoplasmic domain of RANK is useful in
CC developing assays for inhibitors of signal transduction, to screen for
CC molecules that inhibit interaction of RANK with tumour necrosis factor
CC receptor-associated factor (TRAF) 2 or TRAF3. The present sequence is
CC human RANK ligand (RANKL) protein. RANKL gene is located on chromosome 13
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
|
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
|||||||
Db 301 PDQDATYFGAFKVRDID 317

RESULT 10

ABG31631

ID ABG31631 standard; protein; 317 AA.

XX

AC ABG31631;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human RANKL protein.

XX

KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;
KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;
KW dendritic cell activator; T cell enhancer; human; RANKL.

XX

OS Homo sapiens.

XX

PN WO200266044-A2.

XX

PD 29-AUG-2002.

XX

PF 23-OCT-2001; 2001WO-US046254.

XX

PR 24-OCT-2000; 2000US-0242868P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;

XX

DR WPI; 2002-674891/72.

XX

PT Treating an individual with tumors or cancers, e.g. liver cancer or brain
PT tumor, by administering a combination of dendritic cell populations, T
PT cell enhancing factors and activated, antigen-specific T cells.

XX

PS Disclosure; Page 43-44; 44pp; English.

XX

CC The present invention relates to a new method for treating a tumour-
CC bearing subject. The method involves administering a combination of 2 to
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
CC maturation agent, tumour-killing agent, T cell enhancing factor or
CC activated, antigen-specific T cells. The method is useful for treating
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
CC cervical intraepithelial neoplasia. The present amino acid sequence
CC represents the human RANKL protein that was used in the method of the
CC invention

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 11

AAU78285

ID AAU78285 standard; protein; 317 AA.

XX

AC AAU78285;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human TRANCE protein splice variant 1.

XX

KW Human; tumour necrosis factor-related activation induced cytokine;
KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
KW rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea;
KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
KW cartilage growth; skeletal growth.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 126. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 137. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 140. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 145. .317

FT /note= "Specifically claimed in claims 17 and 18"

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FT      Region      158. .317
FT                               /note= "Specifically claimed in claims 17 and 18"
FT      Domain      159. .317
FT                               /note= "TNF core domain, specifically claimed in claims
FT                               17 and 18"
XX
PN      WO200216551-A2.
XX
PD      28-FEB-2002.
XX
PF      20-AUG-2001; 2001WO-US026101.
XX
PR      18-AUG-2000; 2000US-0226197P.
XX
PA      (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
PI      Choi Y,  Odgren PR,  Marks SC;
XX
DR      WPI; 2002-304119/34.
DR      N-PSDB; ABK12876.
XX
PT      Treating mammal having disorder characterized by abnormal
PT      cartilage/skeletal growth such as dwarfism, acromegaly, by administering
PT      tumor necrosis factor-related activation induced cytokine-modulating
PT      agent to mammal.
XX
PS      Disclosure; Fig 10; 55pp; English.
XX
CC      The present invention relates to a new method of treating a mammal having
CC      a disorder comprising insufficient or excessive cartilage or skeletal
CC      growth. The method of the invention involves administering to the mammal
CC      a tumour necrosis factor-related activation induced cytokine (TRANCE)-
CC      modulating agent. The method is useful for treating a mammal having a
CC      disorder comprising insufficient or excessive cartilage or skeletal
CC      growth, where the disorder comprising insufficient cartilage or skeletal
CC      growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal
CC      discrepancies and bone or cartilage damage resulting from traumatic
CC      injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders
CC      comprising excessive cartilage or skeletal growth are selected from
CC      acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and
CC      multiple osteocartilaginous exostoses. The method is useful for
CC      inhibiting chondrocyte differentiation. The present amino acid sequence
CC      represents the human TRANCE protein, splice variant 1, of the invention.
CC      TRANCE is a member of the tumour necrosis factor family and acts directly
CC      on cartilage-producing cells (chondrocytes)
XX
SQ      Sequence 317 AA;

      Query Match      100.0%;  Score 1685;  DB 5;  Length 317;
      Best Local Similarity  100.0%;  Pred. No. 6.5e-154;
      Matches  317;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV  60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV  60

Qy      61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

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Db          |||||
61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||||
Db          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          |||||
Db          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||||
Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy          301 PDQDATYFGAFKVRDID 317
          |||||
Db          301 PDQDATYFGAFKVRDID 317

```

RESULT 12

AAO19096

ID AAO19096 standard; protein; 317 AA.

XX

AC AAO19096;

XX

DT 22-NOV-2002 (first entry)

XX

DE C neoformans antigen expressing dendritic cell related protein #5.

XX

KW Human; fungicide; fungal infection; dendritic cell; antigen;

KW Cryptococcus neoformans; vaccine; immunostimulant.

XX

OS Homo sapiens.

XX

PN WO200266053-A2.

XX

PD 29-AUG-2002.

XX

PF 14-DEC-2001; 2001WO-US048288.

XX

PR 04-JAN-2001; 2001US-0259653P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Thomas EK;

XX

DR WPI; 2002-674896/72.

XX

PT Producing a population of activated, Cryptococcus neoformans antigen-

PT presenting dendritic cells for preventing or treating C. neoformans

PT infection comprises causing the obtained dendritic cells to present the

PT antigen.

XX

PS Disclosure; Page 30-32; 32pp; English.

XX

CC The present invention relates to a method of producing a population of

CC activated, Cryptococcus neoformans antigen-presenting dendritic cells,
CC comprising causing the obtained dendritic cells to present the antigen
CC and maturing the dendritic cells. The activated, C. neoformans antigen-
CC expressing dendritic cells are useful for treating, or as vaccines or
CC vaccine adjuvants against, C. neoformans infection, or for generating
CC antigen-specific T cells. The present sequence is a human protein shown
CC in the exemplification of the invention

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahLTINATDIPSGSH 180
|
Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
|
Db 301 PDQDATYFGAFKVRDID 317

RESULT 13

ADR29336

ID ADR29336 standard; protein; 317 AA.

XX

AC ADR29336;

XX

DT 07-OCT-2004 (first entry)

XX

DE Human RANK-L protein, seq id 6.

XX

KW RANK; receptor activator of NF-kappa B; c-src activity;

KW F-actin ring formation; CaPO 4 resorption; cardiovascular disease;

KW arterial calcification; immune disease; inflammatory disease;

KW toxic shock; septic shock; graft-versus host; vaccine; human; RANK-L.

XX

OS Homo sapiens.

XX

PN WO200224896-A2.

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 ||||||||||||||||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 14

ABP55108

ID ABP55108 standard; protein; 317 AA.

XX

AC ABP55108;

XX

DT 05-FEB-2003 (first entry)

XX

DE Human osteoprotegerin ligand.

XX

KW Osteoprotegerin ligand; OPG ligand; OPGL; human; autoimmune disease;
 KW rheumatoid arthritis; diabetes; osteoarthritis; psoriasis;
 KW inflammatory bowel disease; transplant rejection; allergy;
 KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
 KW antipsoriatic; immunosuppressive; antiallergic; antiinflammatory;
 KW osteopathic; antiulcer; monocyte.

XX

OS Homo sapiens.

XX

Key	Location/Qualifiers
-----	---------------------

FT Domain	1. .47
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FT	/note= "putative cytoplasmic domain"
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FT Domain	48. .68
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FT	/note= "putative transmembrane signal-anchor"
----	---

FT Domain	69. .317
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FT	/note= "putative extracellular domain"
----	--

FT Modified-site	171
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FT	/note= "potential N-glycosylation site"
----	---

FT Modified-site	198
------------------	-----

FT	/note= "potential N-glycosylation site"
----	---

XX

PN WO200276507-A2.

XX

PD 03-OCT-2002.

XX

PF 06-FEB-2002; 2002WO-US001238.

XX

PR 23-MAR-2001; 2001US-0278215P.

XX

PA (GETH) GENENTECH INC.

XX
 PI Grewal I;
 XX
 DR WPI; 2003-058352/05.
 DR N-PSDB; ABV75842.
 XX
 PT Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,
 PT useful for treating immune related disorders such as autoimmune disease,
 PT rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.
 XX
 PS Claim 1; Fig 1B; 111pp; English.
 XX
 CC The present sequence is the protein sequence of human osteoprotegerin
 CC ligand (OPGL), a member of the tumour necrosis factor (TNF) family of
 CC molecules that has been reported to bind to at least 2 receptors, RANK
 CC and OPG. In the present invention, OPGL was shown to activate human
 CC monocytes, and to activate such monocytes to secrete certain cytokines
 CC such as interleukin-1 (IL-1), IL-6, IL-12, MIP-1alpha and TNF-alpha and
 CC chemokines such as IL-8. OPGL may function in up-regulation of co-
 CC stimulatory molecules such as ICAM-a and VCAM-1, LFA, and B7.1, B7.3 and
 CC B7h. OPGL may also serve as an antigen presenting molecule which enhances
 CC T-cell activation. The invention provides methods of using OPGL to
 CC activate monocytes to secrete chemokines or cytokines by exposing a
 CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided
 CC are methods of using OPGL to treat conditions or diseases in mammals
 CC associated with, or resulting from lack of, or decreased, chemokine or
 CC cytokine secretion by monocytes. The invention also provides agonist and
 CC antagonist molecules to modulate immune activity. These may include
 CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti
 CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor
 CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin
 CC is used in a claimed method of treating an immune-related condition,
 CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent
 CC diabetes, osteoarthritis, inflammatory bowel disease (especially
 CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection
 CC or allergy
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.5e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240

Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300
 |||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 15

AAE34364

ID AAE34364 standard; protein; 317 AA.

XX

AC AAE34364;

XX

DT 14-MAY-2003 (first entry)

XX

DE Human receptor activator of NF-kappa B ligand (RANKL).

XX

KW Human; acute septic arthritis; osteomalacia; hyperparathyroidism;
 KW Cushing's syndrome; receptor activator of NF-kappa B ligand; cancer;
 KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;
 KW monoostotic fibrous dysplasia; radiation therapy; spinal cord injury;
 KW RANKL; Gaucher's disease; polyostotic fibrous dysplasia; scurvy.

XX

OS Homo sapiens.

XX

Key	Location/Qualifiers
FT Domain	1. .47
FT	/note= "Intracellular domain"
FT Domain	48. .68
FT	/note= "Transmembrane domain"
FT Domain	69. .317
FT	/note= "Extracellular domain"
FT Binding-site	162. .317
FT	/note= "RANK-binding domain"

XX

PN WO200292016-A2.

XX

PD 21-NOV-2002.

XX

PF 17-MAY-2002; 2002WO-US016002.

XX

PR 17-MAY-2001; 2001US-0291919P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Dougall WC, Anderson DM;

XX

DR WPI; 2003-129220/12.

DR N-PSDB; AAD52598.

XX

PT Treating patients having e.g. acute septic arthritis, osteomalacia,
 PT hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises
 PT administering a receptor activator of NF-kappa B antagonist to increase

PT bone formation.
XX
PS Claim 1; Page 51-52; 52pp; English.
XX
CC The invention relates to a method of treating a patient having e.g. acute
CC septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome
CC or spinal cord injury. The method involves administering a receptor
CC activator of NF-kappa B (RANK) antagonist to stimulate an increase in the
CC rate for formation of new bone. RANK antagonist is capable of inhibiting
CC the ability of RANK to induce NF-kappa B. The method is useful for
CC stimulating bone formation, or for treating patients having acute septic
CC arthritis, osteomalacia (including rickets and scurvy),
CC hyperparathyroidism, Cushing's syndrome, monoostotic fibrous dysplasia,
CC polyostotic fibrous dysplasia, Gaucher's disease, Langerhan's cell
CC histiocytosis, spinal cord injury, patients requiring periodontal
CC reconstruction, or patients who have completed a course or radiation
CC therapy for cancer. The method is also useful for treating a patient who
CC is a prosthetic joint recipient, a bone graft recipient, or a ligament
CC graft recipient. The invention is useful in gene therapy. The present
CC sequence is human RANK ligand (RANKL) protein
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.5e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 171 secs

OM protein - protein search, using sw model

Run on: April 25, 2005, 14:26:55 ; Search time 43 Seconds
 (without alignments)
 550.320 Million cell updates/sec

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 Perfect score: 1685
 Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8					
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2	1685	100.0	317	3	US-08-995-659-13	Sequence 13, Appl	
3	1685	100.0	317	3	US-09-215-649A-13	Sequence 13, Appl	
4	1685	100.0	317	3	US-09-052-521C-4	Sequence 4, Appli	
5	1685	100.0	317	4	US-09-577-780-13	Sequence 13, Appl	
6	1685	100.0	317	4	US-09-577-800-13	Sequence 13, Appl	
7	1685	100.0	317	4	US-09-466-496-13	Sequence 13, Appl	
8	1685	100.0	317	4	US-09-871-856-13	Sequence 13, Appl	
9	1685	100.0	317	4	US-09-871-291-13	Sequence 13, Appl	
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ALIGNMENTS

RESULT 1

US-08-996-139-13

; Sequence 13, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-995-659-13

; Sequence 13, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
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; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-13

Query Match 100.0%; Score 1685; DB 3; Length 317;
 Best Local Similarity 100.0%; Pred. No. 3.9e-163;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-215-649A-13

; Sequence 13, Application US/09215649A

; Patent No. 6271349

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

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; FILING DATE: 17-Dec-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

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;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;          ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;          INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 317 amino acids
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RESULT 4

US-09-052-521C-4

; Sequence 4, Application US/09052521C

; Patent No. 6316408

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors


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; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4
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RESULT 5

US-09-577-780-13

; Sequence 13, Application US/09577780

; Patent No. 6419929

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

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;          CITY: Seattle
;          STATE: WA
;          COUNTRY: USA
;          ZIP: 98101
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: Apple Power Macintosh
;          OPERATING SYSTEM: Apple Operating System 7.5.5
;          SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/995,659
;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2852-A
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;    INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 317 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

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Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 3.9e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240
        |||
Db    181 KVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

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```

                ||||||||||||||||||||||||||||||||||||||||||||
Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy          301 PDQDATYFGAFKVRDID 317
                ||||||||||||||||
Db          301 PDQDATYFGAFKVRDID 317

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RESULT 6

US-09-577-800-13

; Sequence 13, Application US/09577800

; Patent No. 6479635

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/577,800

; FILING DATE: 24-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/996,139

; FILING DATE: 22 DECEMBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid


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;          FILING DATE: 17-Dec-1999
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/996,139
;          FILING DATE: 22 DECEMBER 1997
;          APPLICATION NUMBER: USSN 60/064,671
;          FILING DATE: 14 OCTOBER 1997
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;    INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 317 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-466-496-13

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Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 3.9e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 8

Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 9

US-09-871-291-13

; Sequence 13, Application US/09871291

; Patent No. 6562948

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317

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RESULT 10

US-09-396-937-2

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; Sequence 2, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-396-937-2

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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RESULT 11

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. 6649164

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12
 US-09-865-363-13


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; ATTORNEY/AGENT INFORMATION:
;   NAME: Perkins, Patricia Anne
;   REGISTRATION NUMBER: 34,693
;   REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206)587-0430
;   TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 317 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-688-459-13
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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 14

US-08-842-842-7

; Sequence 7, Application US/08842842

; Patent No. 5843678

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California


```
Qy      240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEIEISIEVSNPSLL 299
        ||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| : |||||
Db      239 VYVVKTSIKIPSSHNLKGGSTKNWSGNSEFHFYSINVGGFCKLRAGEEISIQVSNPSLL 298

Qy      300 DPDQDATYFGAFKVRDID 317
        ||||| ||||| : |||
Db      299 DPDQDATYFGAFKVQDID 316
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Search completed: April 25, 2005, 14:34:33
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 14:33:01 ; Search time 41 Seconds
(without alignments)
743.920 Million cell updates/sec

Title: US-09-211-315-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	234	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	235	2	I54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	tumor necrosis fac
12	130.5	7.7	306	2	I49139	lymphotoxin-beta -
13	130	7.7	233	1	S22052	tumor necrosis fac

14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	CD40 ligand - mous
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta -
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	lymphotoxin alpha
25	92.5	5.5	450	2	S38114	hypothetical prote
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF3526	homoproteocatechua
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A49733	[heparan sulfate]-
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHU7L	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

ALIGNMENTS

RESULT 1

I38707

Fas ligand - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C;Accession: I38707; JC2340; S57565; I38554

R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A;Reference number: I38707; MUID:95127560; PMID:7826947

A;Accession: I38707

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-281 <RES>

A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Kamada, T.

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;
Best Local Similarity 21.7%; Pred. No. 2.2e-08;
Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

```

Qy      22 PGAPHEGPLHAPPPAP----HQPPAASRS-----MFVALLGLGLGQVVCS 63
      | |  ||  ||| |      || |      : |||:||||
Db      46 P P P P P P P L P P P P P P L P L P L P L K K R G N H S T G L C L L V M F F M V L V A L V G L G L G ---- 100

Qy      64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF 123
      :| | |      | | : : : | :
Db     101 --MFQLFHLQ-----KELAE LRESTSQMHTA----- 124

Qy     124 QGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPF AHLT--INATDIPSGSHK 181
      : : : : |      | | : ||| | | : : |
Db     125 -SSLEKQIGH-----PSPPEKKELRKVAHLTGKSNSRSMP----- 159

Qy     182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVY 241
      |      | : | : : | | : : | | : : | | :      | |
Db     160 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----LPLSHK 210

Qy     242 VTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVG GFFKLRS GEEISIEVSN 295
      | : | | : : |      | : : |      : | | | : : : | |
Db     211 VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----YLGAVFNLT SADHLYVNVSE 263

```

Qy 296 PSLLDPDQDATYFGAFKV 313
||:: :: |:| :|:
Db 264 LSLVNFEEESQTFFGLYKL 281

RESULT 2

A53062

Fas ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: A53062

R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagata, S.

Cell 76, 969-976, 1994

A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.

A;Reference number: A53062; MUID:94185175; PMID:7511063

A;Accession: A53062

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-279 <TAK>

A;Cross-references: UNIPROT:P41047; GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.9%; Score 184.5; DB 2; Length 279;
Best Local Similarity 21.7%; Pred. No. 5.3e-08;
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPHAPPPAPHQP-----PAASRSMFVALLGLGL 57
|| :: | | || | | | | : |||:|:
Db 38 RGPDQRRPPPPPPVSPPLPPSQPLPLPPLTPLKKKDHTNLWLPVVFVVLVALVGMGL 97

Qy 58 GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
| :|:: |
Db 98 G-----MYQLFHL----- 105

Qy 118 RIKQAFQGAVQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINA 172
||| : :| :: || : : | | : ||| |
Db 106 -----QKELAELEFETNQSLKVSSFEEKQIANPS----TPSEKKEPRSVAHLTGN- 150

Qy 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
| | : | | || : : | |::| : |::| : : | :
Db 151 -----PHRSIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN--- 201

Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEESISI 291
: | ||: : | | ||: | : : :| :| | | : : :
Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGAVFNLTADHLYV 257

Qy 292 EVSNPSLLDPDQDATYFGAFKV 313
:| ||:: :: |:| :|:
Db 258 NISQLSLINFEEESKTFFGLYKL 279

RESULT 3

S53090

CD40 ligand - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C;Accession: S53090
 R;Mertens, B.E.L.C.; Muriuki, M.
 submitted to the EMBL Data Library, February 1995
 A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
 A;Reference number: S53090
 A;Accession: S53090
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-261 <MER>
 A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1;
 PID:g732570

Query Match 10.5%; Score 176.5; DB 2; Length 261;
 Best Local Similarity 24.2%; Pred. No. 2.3e-07;
 Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

```

Qy      33 PPPPAPHQPPAASRSMFVALLGLGL-GQVVCVALFFYFRAQMDPNRISEDGTHCIYRIL 91
      | | :   | | :|: || : | |:: |   |   ::| :| ::
Db      8 PPSRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R 57

Qy      92 RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG 149
      |||: | |   : |   :| | : | : | : |   :: :: :: :
Db      58 NLHEDFVFMKTIQRCNKGEGLSLLNCEEIRSRFEDLVKDIMQ---NKEVKKKEKNFE- 112

Qy     150 SWLDLAKRSKLEAQPF AHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-L 206
      :   | | ||: | :   |   | : |   :| :| :| || |
Db     113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYTSLNNLVTLENGKQL 161

Qy     207 IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264
      | : |||:| : | :   | |   : :   :| | | | : : |
Db     162 AVKRQGFYYIYTQVTFCNSR-----ETLSQAPFIASLCLKSPSGSERILLRAANTH-- 212

Qy     265 SGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
      | :   ||::|| |::|| : : |::|| :   | || | :
Db     213 SSSKPCGQQSIHLGGVFELQSGASVFNVTDP SQVSHGTGFTSFGLLKL 261

```

RESULT 4

A49266

fas ligand - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: A49266

R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.

Cell 75, 1169-1178, 1993

A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.

A;Reference number: A49266; MUID:94084792; PMID:7505205

A;Accession: A49266

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-278 <SUD>

A;Cross-references: UNIPROT:P36940; GB:U03470; NID:g440178; PIDN:AAC52129.1;

PID:g440179

C;Keywords: glycoprotein; transmembrane protein

```

Query Match      10.4%; Score 175.5; DB 2; Length 278;
Best Local Similarity 20.3%; Pred. No. 3e-07;
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

Qy      21 GPGAPHEGPLHAPPPAPHQPPAASRSM-----FVALLGLGL 57
      |||      |      ||||:|  ||:      :      |||:|:|
Db      39 GPGQRRPPP--PPPPSPLPSPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96

Qy      58 GQVVCVSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
      |      ::      |      :      :      |      :      :      :      |      |::      :      :
Db      97 G-----MYQLFHLQKELAELEFNTNHSLE-RVSSFEKQIANPSTPSETKKPRSV----- 143

Qy     118 RIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPS 177
                        |||| |
Db     144 -----AHLTGNPR----- 151

Qy     178 GSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
      |      :      |      |      ||      :      :      |      |::|:      |      |::|:      :      ||      :      ::      |
Db     152 -SRSIPL-EWEDTYGTALISGVK YKKGGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205

Qy     238 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPS 297
      ||:      :      |      ||      ||:      |      :      :      :      |      :      |      |      :      :      :      :      |      |
Db     206 HKVYM--RNFKYPGDLVLMEKKLNYCT-TGQIWAHSSYLGA VFNLT VADHLYVNISQLS 262

Qy     298 LLDPDQDATYFGAFKV 313
      |::      ::      |::|      ::
Db     263 LINFEESKTFFGLYKL 278

```

A;Residues: 1-261 <SPR>
 A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
 A;Experimental source: peripheral blood T-cell
 R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.
 Eur. J. Immunol. 22, 3191-3194, 1992
 A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A;Reference number: S26694; MUID:93076854; PMID:1280226
 A;Accession: S26694
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-261 <GRA>
 A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.;
 Bonnefoy, J.Y.
 FEBS Lett. 315, 259-266, 1993
 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and
 regulation of expression by factors controlling IgE production.
 A;Reference number: S28852; MUID:93138085; PMID:7678552
 A;Accession: S28852
 A;Molecule type: mRNA
 A;Residues: 1-261 <GAU>
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having
 6-Gln
 C;Genetics:
 A;Gene: GDB:CD40LG; HIGM1; IMD3
 A;Cross-references: GDB:120632; OMIM:308230
 A;Map position: Xq26-Xq26
 C;Keywords: glycoprotein; transmembrane protein
 F;13-44/Domain: transmembrane #status predicted <TMM>
 F;45-261/Domain: extracellular #status predicted <EXT>
 F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;
 Best Local Similarity 24.5%; Pred. No. 7.7e-06;
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

```

Qy      45 SRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT- 102
      |  :: || : |  :: |  :: |  :: |  :: |  :: |  :: |  :: |  :: |
Db      20 SMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----RNLHEDFVFMKTI 69

Qy     103 -TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLE 161
      : : |  : |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      70 QRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEETKKENSF-EMQKGDQ-N 119

Qy     162 AQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA 218
      |  ||:  |:  |  |:  |  :::  :||  :|  |||  |  |  :  |  ||:  ||
Db     120 PQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKROGLYYIYA 173

Qy     219 NICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
      : |  :  :  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     174 QVTFCNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSAKPCGQQSIH 224

Qy     277 VGGFFKLRSGEESISIEVSNPSLLDPDQDATYFGAFKV 313
      :||  ||:  |  :  :  ||:  ||  :  |  ||  ||
Db     225 LGGVFELQPGASVFVNVTDPQVSHGTGFTSFGLLKL 261
  
```

RESULT 6

QWMSN

tumor necrosis factor alpha precursor - mouse

N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.

DNA 7, 193-201, 1988

A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.

A;Reference number: A22908; MUID:88224564; PMID:2836146

A;Accession: A22908

A;Molecule type: DNA

A;Residues: 1-235 <SHI>

A;Cross-references: UNIPROT:P06804; GB:M20155

R;Shakhov, A.N.; Nedospasov, S.A.

Bioorg. Khim. 13, 701-705, 1987

A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence of the genomic copy of TNF-alpha in mice.

A;Reference number: S03791; MUID:87298639; PMID:3040015

A;Accession: S03791

A;Molecule type: DNA

A;Residues: 1-235 <SHA>

A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087

A;Note: article in Russian with English abstract

R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha- (tumor necrosis factor) and TNF-beta- (lymphotoxin) genes.

A;Reference number: A93679; MUID:88067722; PMID:3684584

A;Accession: A27303

A;Molecule type: DNA

A;Residues: 1-235 <SEM>

A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor.

A;Reference number: A25164; MUID:85298296; PMID:3898078

A;Accession: A25164

A;Molecule type: mRNA

A;Residues: 1-235 <PEN>

A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085

R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.;

Kawashima, E.; Chollet, A.; Tizard, R.; van Heuverswyn, H.; van Vliet, A.;

Ruysschaert, M.R.; Fiers, W.

Nucleic Acids Res. 13, 4417-4429, 1985

A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.

A;Reference number: A23127; MUID:85242112; PMID:2989794

A;Accession: A23127

A;Molecule type: mRNA

A;Residues: 1-235 <FRA>

A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R;Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted protein.
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A. Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of mRNA molecules specifying inflammatory mediators.
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A. Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor.
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141.5; DB 1; Length 235;
Best Local Similarity 25.9%; Pred. No. 0.00018;
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |           |:|           | | :|| | : :|| || | :|: :
Db      90 KPAHVVAN-----HQVEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLVSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:      |      :|: |      |::           :|| |      :| | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW---- 192

Qy      269 EFHFYSINVGGFFKLRSGEISIEVSNPSLLD-PDQDATYFG 309
          : | :|| |:| |::| ||: | || :      |||
Db      193 ---YEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFG 231

```

RESULT 7
A25451
tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A25454; A25451; JS0727
 R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.; Kato, M.; Seko, M.
 DNA 5, 149-156, 1986
 A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor.
 A;Reference number: A25454; MUID:86219711; PMID:3519137
 A;Accession: A25454
 A;Molecule type: mRNA
 A;Residues: 1-234 <ITO>
 A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A;Reference number: A25451; MUID:86219712; PMID:3519138
 A;Accession: A25451
 A;Molecule type: DNA
 A;Residues: 1-234 <IT2>
 A;Note: this sequence differs from that shown in having a Gln inserted between residues 62 and 63
 R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A. Gene 95, 215-221, 1990
 A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).
 A;Reference number: JH0309; MUID:91065534; PMID:2249779
 A;Accession: JS0727
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-62,'Q',63-234 <SHA>
 A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C;Genetics:
 A;Introns: 62/3; 80/1; 96/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
 F;1-81/Domain: propeptide #status predicted <PRO>
 F;82-234/Product: tumor necrosis factor #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;147-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;
 Best Local Similarity 21.6%; Pred. No. 0.0002;
 Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;

```

Qy      27 EGPLHAPPPAPHQPPAASR----SMFVALLGLGLGQVVCSSVALFFYFRAQMDPNRISED 82
        ||| |   |   |   : |   |:| || |   : |   :||   | :
Db      14 EGPL----PKKAGGPQGSKRCLCLSLFSFLLVAGATTLFC----LLHFRVIGPQEEESP 65

Qy      83 GTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRA 142
        | :       |   |   || |

```

```

Db          66 NLHLV-----NPVAQMVTLS-----A 82
Qy          143 EKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTF 201
           :: |          :| ||: |      |      ::      |      |      ::| |
Db          83 SRALSD-----KPLAHVVAN----PQVEGQL---QWLSQRANALLANGMKL 121
Qy          202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--- 258
           :: ::| |  | ::: |      ||      | : |  |:: :: | :  | :
Db          122 TDNQLVVPADGLYLIYSQVLF-----SGQGCRSYVLLTHTVSRFAVSYPNKVNLLSAIKS 176
Qy          259 -----GSTKYWSGNSEFHFYSINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYF 308
           |          : | :|| |:|  | : :| ||: |  ||  :      ||
Db          177 PCHRETPEEAEPMAW-----YEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYF 229
Qy          309 G 309
           |
Db          230 G 230

```

RESULT 8

JH0529

tumor necrosis factor alpha precursor - sheep

N;Alternate names: cachectin; TNF alpha

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JH0529; S48118; S13114; S20661

R;Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.

A;Reference number: JH0529; MUID:92112044; PMID:1765267

A;Accession: JH0529

A;Molecule type: mRNA

A;Residues: 1-234 <GRE>

A;Cross-references: UNIPROT:P23383; EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A;Experimental source: alveolar macrophage

R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A;Reference number: S48118; MUID:92155784; PMID:1786996

A;Accession: S48118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-234 <NAS>

A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A;Reference number: S13114; MUID:91067496; PMID:2251151

A;Accession: S13114

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-62,64-234 <YOU>

A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A;Note: comparison with the introns of homologous sequences suggest that this is probably an alternative splicing

C;Superfamily: tumor necrosis factor
C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein;
lipoprotein; lymphokine; macrophage; myristylation; transmembrane protein
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Qy	134	IVGSQHIRAEKAMVDGSW---LDLAKRSKLEA---QPPFAHLTINATDIPSGSHKVSLSW	187
		:: :: : : :	::
Db	55	VIGPQ--REEQSPAGPSFNRPLVQTLRSSSQASNNKPVAHVVAN-----ISAP	100
Qy	188	YHDRGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDL	231
		: : : : : : :	:
Db	101	GQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRI	160
Qy	232	ATEYLQLMVVYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEIISI	291
		: : : : : : :	
Db	161	AVSY-QTKVNIL-SAIKSPCHRETLEGAEAKPW-----YEPIYQGGVFQLEKGDRLSA	211
Qy	292	EVSNPSSLDD-PDQDATYFG	309
		:: :	
Db	212	EINLPEYLDYAESGOVYFG	230

A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-233 <IRI>
 A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.; Kohr, W.J.; Aggarwal, B.B.; Goeddel, D.V.
 Nature 312, 724-729, 1984
 A;Title: Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin.
 A;Reference number: A93351; MUID:85086244; PMID:6392892
 A;Accession: A93351
 A;Molecule type: mRNA
 A;Residues: 1-233 <PEN>
 A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelocytic leukemia
 R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Yamamoto, R.; Mark, D.F.
 Science 228, 149-154, 1985
 A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A;Reference number: A44189; MUID:85142190; PMID:3856324
 A;Accession: A44189
 A;Molecule type: mRNA
 A;Residues: 1-62,'S',64-233 <WAN>
 A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
 R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.; Sugimoto, T.; Kurimoto, M.
 Lymphokine Res. 7, 175-185, 1988
 A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and interferon-alpha from BALL-1 cells stimulated by HVJ.
 A;Reference number: A61478; MUID:88301617; PMID:2841543
 A;Accession: B61478
 A;Molecule type: protein
 A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,'X',182-204 <FUK>
 R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.
 Eur. J. Biochem. 152, 515-522, 1985
 A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison with mouse tumor necrosis factor.
 A;Reference number: I53311; MUID:86030296; PMID:3932069
 A;Accession: I53311
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <MAR>
 A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
 A;Experimental source: U-937 cells
 R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
 A;Reference number: S62610; MUID:96202967; PMID:8631363
 A;Accession: S62610
 A;Molecule type: protein

A;Residues: 77-99 <TAK>
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region.
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues.
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringman, T.S.; Nedwin, G.E.; Goeddel, D.V.; Harkins, R.N.
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction, TNF-alpha can cause cytolysis of certain tumor cell lines and have an antiproliferative effect on others without detriment to normal cells. It can also act synergistically with interferon gamma to kill certain transformed cell lines.
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;
Best Local Similarity 25.5%; Pred. No. 0.00094;
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

```
Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
          :| ||: |   |   ::   | : | | ::| :   : :|| : | | :| : :
Db      87 KPAHVVAN----PQAEQQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139

Qy      222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
```

```

      |:      :: | | : : | | | :|| | :| | | :
Db      140 FKGQGPCSTHVLTLTHTISRIASVYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      | :|| |:| |: :| |: : | | | : | ||
Db      193 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 229

```

RESULT 10

I54490
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from
Peromyscus leucopus (family Cricetidae).
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA40596.1;
PID:g202507
C;Genetics:
A;Gene: PlTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

```

Query Match          7.9%; Score 132.5; DB 2; Length 235;
Best Local Similarity 25.3%; Pred. No. 0.0011;
Matches 42; Conservative 27; Mismatches 54; Indels 43; Gaps 7;

```

```

Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMTFSNG-----KLIVNQDGFYYL 216
      :| ||: |      |:| : || :| :|| :||: || | :
Db      90 KPAHVVAN-----HQVDEQLEWLSRG----ANALLANGMDLKDNLVIPADGLYLV 137

Qy      217 YANICFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYW 264
      |: : |: | : |: | |: : :|| | :| | |
Db      138 YSQVLFK-----GQGCSSYVLLTHTVSRFAVSYEDKVNLLSAIKSPCPKETPEGSELKPW 192

Qy      265 SGNSEFHFYSINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      : | :|| |:| |: :| ||: | || : | ||
Db      193 -----YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

```

RESULT 11

JU0029
tumor necrosis factor alpha precursor - rat
N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0029; JN0868; S21674

R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
 Agric. Biol. Chem. 53, 1733-1736, 1989
 A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.
 A;Reference number: JU0029
 A;Accession: JU0029
 A;Molecule type: DNA
 A;Residues: 1-235 <SHI>
 A;Cross-references: UNIPROT:P16599
 R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
 Gene 132, 227-236, 1993
 A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
 A;Reference number: JN0868; MUID:94040766; PMID:8224868
 A;Accession: JN0868
 A;Molecule type: DNA
 A;Residues: 1-235 <KWO>
 A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254
 R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
 Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
 A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.
 A;Reference number: S21674; MUID:92329007; PMID:1627266
 A;Accession: S21674
 A;Molecule type: mRNA
 A;Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>
 A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
 C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and produces hemorrhagic necrosis of tumors.
 C;Genetics:
 A;Gene: TNF-alpha
 A;Introns: 62/3; 81/1; 97/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
 F;80-235/Product: tumor necrosis factor #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;
 Best Local Similarity 25.3%; Pred. No. 0.0013;
 Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVSLs-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |           |:      |  |  | :|| |   : :||: .|| | :|: :
Db      90 KPAHVVAN-----HQAEQLEWLSQRANALLANGMDLKDNLVVPADGLYLIYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:      |   :|: |   |:      :|| |   :|  | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPW---- 192

Qy      269 EFHFYSINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          :  : :|| |:|  |: :| ||: |  ||  :   |||
Db      193 ---YEPMYLGGVFQLEKGDLLSAEVNLPKYLDITESGQVYFG 231

```


RESULT 12

I49139

lymphotoxin-beta - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49139; I49138; I49076

R;Lawton, P.; Nelson, J.; Tizard, R.; Browning, J.L.

J. Immunol. 154, 239-246, 1995

A;Title: Characterization of the mouse lymphotoxin-beta gene.

A;Reference number: I49138; MUID:95088371; PMID:7995944

A;Accession: I49139

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-306 <RES>

A;Cross-references: UNIPROT:P41155; EMBL:U16985; NID:g577830; PIDN:AAA70089.1; PID:g577831

A;Accession: I49138

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-306 <RE3>

A;Cross-references: EMBL:U16984; NID:g577431; PIDN:AAB60493.1; PID:g577432

R;Pokholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov, S.V.; Novobrantseva, T.I.; Turetskaya, R.L.; Green, J.E.; Nedospasov, S.A. Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995

A;Title: Cloning and expression analysis of the murine lymphotoxin beta gene.

A;Reference number: A55602; MUID:95148600; PMID:7846035

A;Accession: I49076

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-306 <RE2>

A;Cross-references: EMBL:U12029; NID:g515508; PIDN:AAA67716.1; PID:g515509

C;Genetics:

A;Gene: LT-beta

A;Introns: 54/3; 160/1

Query Match 7.7%; Score 130.5; DB 2; Length 306;

Best Local Similarity 22.1%; Pred. No. 0.0022;

Matches 55; Conservative 38; Mismatches 87; Indels 69; Gaps 12;

```

Qy      105 ESQDTKLIP---DSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLE 161
      | : | : | | : : | : | | | | | | | | | | | | | | | | | | | | | |
Db      86 ETPDPRLHPQRSNASRNLASTSQGPV-----AQSSREASAWMTI----- 124

Qy      162 AQPFAHLTIN--ATDIPSGSHKVSL-----SWYHDRG--WAKISNMTF----- 201
      | | | | : : | | : | : : | | : | | | | | | | | | | | | | |
Db      125 LSPAADSTPDPGVQQLPKGEPETDLNPPLPAHLIGAWMSGQGLSWEASQEEAFLRSGAQ 184

Qy      202 ---SNGKLIVNQDGFYYLYANICFR-HHETSGDLATEYLQL--MVYVTKTSIKIPSSHTL 255
      : : | | : | | | | | | | : : | | : | | | | | | | | | | | |
Db      185 FSPTHG-LALPDGVIYLYCHVGYRGRTTPAGRSRARSLLRSALYRAGGAYGRGSPPELL 243

Qy      256 MKGGST-----KYWSGNSEHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQD 304
      : : | | | | | | | | | | : | : | | | | | | | | | | | | |
Db      244 LEGAETVTPVVDPIGYGSLW-----YTSVGFGLAQLRSGERVYVNISHPDMVDYRRG 296

```

Qy 305 ATYFGAFKV 313
|:| | |
Db 297 KTFFGAVMV 305

RESULT 13

S22052

tumor necrosis factor alpha precursor - baboon

C;Species: Papio sp. (baboon)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S22052

R;Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A;Reference number: S22052

A;Accession: S22052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <SAN>

A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1;

PID:g38160

C;Genetics:

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 7.7%; Score 130; DB 1; Length 233;
Best Local Similarity 25.5%; Pred. No. 0.0017;
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
:| |: | : : | : | :| : : |:| :| | :| :
Db 87 KPAHVVAN----PQAEQQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139

Qy 222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
|: : : | | : : | | :| | :| | :
Db 140 FKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy 274 SINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
| :| | :| | : :| | : | | :
Db 193 PIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229

RESULT 14

JQ1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JQ1344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.
 A;Reference number: JQ1344; MUID:92084125; PMID:1748301
 A;Accession: JQ1344
 A;Molecule type: DNA
 A;Residues: 1-234 <SUX>
 A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
 C;Comment: This protein is an important proximal mediator of endotoxemia.
 C;Genetics:
 A;Gene: TNF-alpha
 A;Introns: 62/3; 79/1; 95/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
 F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;146-178/Disulfide bonds: #status predicted

Query Match 7.6%; Score 128; DB 1; Length 234;
 Best Local Similarity 24.2%; Pred. No. 0.0025;
 Matches 39; Conservative 32; Mismatches 58; Indels 32; Gaps 8;

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Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
          :| ||: |   |   ::   |   |   ||: :   :: ||: || | :|: :
Db      88 KPAHVVAN----PQAEQQL---QWLSGRANALLANGVKLTNDQLVVPLDGLYLIYSQVL 140

Qy      222 FRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG-----GSTKYWSGNSE 269
          |:   |   :|   |   :: ::   ||   |   |   |   |
Db      141 FK---QGQCPSTHVL-LTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPW----- 191

Qy      270 FHFYSINVGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          : | :|| |:| |::| |:: |: || :   |||
Db      192 --YEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFG 230
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RESULT 15

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 7.5%; Score 126.5; DB 1; Length 233;

Best Local Similarity 25.5%; Pred. No. 0.0033;

Matches 50; Conservative 25; Mismatches 80; Indels 41; Gaps 9;

Qy 134 IVGSQH IRAEKAMVDG SWLDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSWYHD 190
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Db 55 VIGPQREESPGGPSINSPLVQTLRSSSQASSNKPVAHV---VADINSPGQL----- 102

Qy 191 RGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDLATE 234
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Db 103 RWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFRGQGPCSTPLFLTHTISRIAVS 162

Qy 235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVS 294
| | | : :|| | : | | : | | | :| :| :| :|

Db 163 Y-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYQGGVFQLEKGDRLSAEIN 213

Qy 295 NPSLLD-PDQDATYFG 309
| | | : || |

Db 214 LPDYLDYAESGQVYFG 229

Search completed: April 25, 2005, 14:45:58

Job time : 43 secs

OM protein - protein search, using sw model

Run on: April 25, 2005, 14:30:00 ; Search time 135 Seconds
(without alignments)
781.443 Million cell updates/sec

Title: US-09-211-315-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1685	100.0	317	9	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	9	US-09-871-856-13	Sequence 13, Appl
3	1685	100.0	317	9	US-09-957-944-6	Sequence 6, Appli
4	1685	100.0	317	9	US-09-865-363-13	Sequence 13, Appl
5	1685	100.0	317	9	US-09-871-291-13	Sequence 13, Appl
6	1685	100.0	317	9	US-09-877-650-13	Sequence 13, Appl
7	1685	100.0	317	11	US-09-933-915A-2	Sequence 2, Appli
8	1685	100.0	317	14	US-10-151-071-10	Sequence 10, Appl
9	1685	100.0	317	14	US-10-218-547-22	Sequence 22, Appl
10	1685	100.0	317	14	US-10-405-878-13	Sequence 13, Appl
11	1685	100.0	317	14	US-10-167-182-11	Sequence 11, Appl
12	1685	100.0	317	14	US-10-310-793-28	Sequence 28, Appl
13	1685	100.0	317	15	US-10-460-623-11	Sequence 11, Appl
14	1685	100.0	317	15	US-10-289-456-79	Sequence 79, Appl
15	1685	100.0	317	15	US-10-202-062-22	Sequence 22, Appl
16	1685	100.0	317	16	US-10-664-801-2	Sequence 2, Appli
17	1685	100.0	317	16	US-10-381-160-6	Sequence 6, Appli
18	1685	100.0	317	16	US-10-802-133-13	Sequence 13, Appl
19	1685	100.0	317	16	US-10-825-898-4	Sequence 4, Appli
20	1685	100.0	317	16	US-10-854-300-11	Sequence 11, Appl
21	1685	100.0	317	17	US-10-129-595-1	Sequence 1, Appli
22	1685	100.0	317	17	US-10-451-200-6	Sequence 6, Appli
23	1424.5	84.5	316	9	US-09-957-944-8	Sequence 8, Appli
24	1422	84.4	270	15	US-10-289-456-80	Sequence 80, Appl
25	1417.5	84.1	316	10	US-09-079-569-7	Sequence 7, Appli
26	1417.5	84.1	316	10	US-09-873-829-4	Sequence 4, Appli
27	1417.5	84.1	316	11	US-09-933-915A-16	Sequence 16, Appl
28	1417.5	84.1	316	13	US-10-017-910-4	Sequence 4, Appli
29	1417.5	84.1	316	14	US-10-105-057-2	Sequence 2, Appli
30	1417.5	84.1	316	14	US-10-272-411-19	Sequence 19, Appl
31	1417.5	84.1	316	14	US-10-272-328A-19	Sequence 19, Appl
32	1417.5	84.1	316	14	US-10-326-052-2	Sequence 2, Appli
33	1417.5	84.1	316	14	US-10-167-182-1	Sequence 1, Appli
34	1417.5	84.1	316	15	US-10-460-623-1	Sequence 1, Appli
35	1417.5	84.1	316	16	US-10-664-801-4	Sequence 4, Appli
36	1417.5	84.1	316	16	US-10-664-801-6	Sequence 6, Appli
37	1417.5	84.1	316	16	US-10-825-898-2	Sequence 2, Appli
38	1417.5	84.1	316	16	US-10-854-300-1	Sequence 1, Appli
39	1326.5	78.7	294	9	US-09-871-856-11	Sequence 11, Appl
40	1326.5	78.7	294	9	US-09-865-363-11	Sequence 11, Appl
41	1326.5	78.7	294	9	US-09-871-291-11	Sequence 11, Appl
42	1326.5	78.7	294	9	US-09-877-650-11	Sequence 11, Appl
43	1326.5	78.7	294	14	US-10-405-878-11	Sequence 11, Appl
44	1326.5	78.7	294	16	US-10-802-133-11	Sequence 11, Appl
45	1325	78.6	250	15	US-10-338-785A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-813-329-7

; Sequence 7, Application US/09813329

; Patent No. US20020012968A1

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; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor
Class Molecule ("DmTNF") and
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7
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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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RESULT 2

US-09-871-856-13

; Sequence 13, Application US/09871856

; Patent No. US20020081720A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

```

;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Immunex Corporation, Law Department
;      STREET: 51 University Street
;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/871,856
;      FILING DATE: 31-May-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/996,139
;      FILING DATE: <Unknown>
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2851-A
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

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Query Match          100.0%;  Score 1685;  DB 9;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 3.7e-149;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
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Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
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Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|

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Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
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Db 301 PDQDATYFGAFKVRDID 317

RESULT 3

US-09-957-944-6

; Sequence 6, Application US/09957944
 ; Publication No. US20020086312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dougall, William C.
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR
 ACTIVATOR OF
 ; TITLE OF INVENTION: NF-kappa B
 ; FILE REFERENCE: 3109-A
 ; CURRENT APPLICATION NUMBER: US/09/957,944
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: 60/235,157
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-957-944-6

Query Match 100.0%; Score 1685; DB 9; Length 317;
 Best Local Similarity 100.0%; Pred. No. 3.7e-149;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

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Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

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Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

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Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

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Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
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RESULT 4

US-09-865-363-13

; Sequence 13, Application US/09865363

; Publication No. US20020086826A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/865,363

; FILING DATE: 25-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-865-363-13

Query Match 100.0%; Score 1685; DB 9; Length 317;

Best Local Similarity 100.0%; Pred. No. 3.7e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 |||
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
 |||
 Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
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 Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

US-09-871-291-13

; Sequence 13, Application US/09871291

; Publication No. US20020086827A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

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; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 6

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. US20020169117A1

GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19


```

Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 7

US-09-933-915A-2

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; Sequence 2, Application US/09933915A
; Publication No. US20040247596A1
; GENERAL INFORMATION:
; APPLICANT: Odgren, Paul R.
; APPLICANT: Marks, Sandy C.
; APPLICANT: Choi, Yongwon
; TITLE OF INVENTION: TRANCE REGULATION OF CHONDROCYTE
; TITLE OF INVENTION: DIFFERENTIATION
; FILE REFERENCE: 07917-120001
; CURRENT APPLICATION NUMBER: US/09/933,915A
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/226,197
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-915A-2

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Query Match          100.0%; Score 1685; DB 11; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Qy      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

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RESULT 9

US-10-218-547-22
; Sequence 22, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relating To
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 317
; TYPE: PRT
; ORGANISM: human
US-10-218-547-22

Query Match 100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 10
US-10-405-878-13
; Sequence 13, Application US/10405878
; Publication No. US20030175840A1
; GENERAL INFORMATION:


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;      APPLICANT: Anderson, Dirk M.
;      Galibert, Laurent
;      Maraskovsky, Eugene
;      TITLE OF INVENTION: Receptor Activator of NF-kappaB
;      NUMBER OF SEQUENCES: 19
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Immunex Corporation, Law Department
;      STREET: 51 University Street
;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/405,878
;      FILING DATE: 01-Apr-2003
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/996,139
;      FILING DATE: 22 DECEMBER 1997
;      APPLICATION NUMBER: USSN 60/064,671
;      FILING DATE: 14 OCTOBER 1997
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2851-A
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-405-878-13

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Query Match          100.0%;  Score 1685;  DB 14;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 3.7e-149;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|

Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|

```

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSH 180
 |||
 Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSH 180

Qy 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 11

US-10-167-182-11

; Sequence 11, Application US/10167182
 ; Publication No. US20030176647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamaguchi, Kyoji
 ; APPLICANT: Yasuda, Hisataka
 ; APPLICANT: Nakagawa, No. US20030176647Aluaki
 ; APPLICANT: Shima, No. US20030176647Aluyuki
 ; APPLICANT: Kinoshita, Masahiko
 ; APPLICANT: Tsuda, Eisuke
 ; APPLICANT: Goto, Masaaki
 ; APPLICANT: Yano, Kazuki
 ; APPLICANT: Tomoyasu, Akihiro
 ; APPLICANT: Kobayashi, Fumie
 ; APPLICANT: Washida, Naohiro
 ; APPLICANT: Takahashi, Ken
 ; APPLICANT: Morinaga, Tomonori
 ; APPLICANT: Higashio, Kanji
 ; TITLE OF INVENTION: Antibodies to OCIF-binding Molecules
 ; FILE REFERENCE: FJN-070DV
 ; CURRENT APPLICATION NUMBER: US/10/167,182
 ; CURRENT FILING DATE: 2002-06-11
 ; PRIOR APPLICATION NUMBER: US 09/202,455
 ; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: JP 97808/1997
 ; PRIOR FILING DATE: 1997-04-15
 ; PRIOR APPLICATION NUMBER: JP 151434/1997
 ; PRIOR FILING DATE: 1997-06-09
 ; PRIOR APPLICATION NUMBER: JP 217897/1997
 ; PRIOR FILING DATE: 1997-08-12
 ; PRIOR APPLICATION NUMBER: JP 224803/1997
 ; PRIOR FILING DATE: 1997-08-21
 ; PRIOR APPLICATION NUMBER: JP 332241/1997
 ; PRIOR FILING DATE: 1997-12-02
 ; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-182-11

Query Match 100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 12

US-10-310-793-28

; Sequence 28, Application US/10310793

; Publication No. US20030198640A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A

; APPLICANT: Zhang, Jun

; APPLICANT: Wei, Ping

; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases

; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta

; FILE REFERENCE: PF573

; CURRENT APPLICATION NUMBER: US/10/310,793

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 60/336,695

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 10/226,294

; PRIOR FILING DATE: 2002-08-23

; PRIOR APPLICATION NUMBER: 60/314,381

; PRIOR FILING DATE: 2001-08-24

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; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: human
US-10-310-793-28

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Query Match          100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Qy    121 QAFQGA VQKELQHIVGSQHIRA EKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
|
Db    121 QAFQGA VQKELQHIVGSQHIRA EKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
|
Qy    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|
Db    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|
Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Qy    301 PDQDATYFGAFKVRDID 317
|
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 13
US-10-460-623-11
; Sequence 11, Application US/10460623
; Publication No. US20030208045A1
; GENERAL INFORMATION:

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; APPLICANT: Yamaguchi, Kyoji
; APPLICANT: Yasuda, Hisataka
; APPLICANT: Nakagawa, No. US20030208045Aluaki
; APPLICANT: Shima, No. US20030208045Aluyuki
; APPLICANT: Kinosaki, Masahiko
; APPLICANT: Tsuda, Eisuke
; APPLICANT: Goto, Masaaki
; APPLICANT: Yano, Kazuki
; APPLICANT: Tomoyasu, Akihiro
; APPLICANT: Kobayashi, Fumie
; APPLICANT: Washida, Naohiro
; APPLICANT: Takahashi, Ken
; APPLICANT: Morinaga, Tomonori
; APPLICANT: Higashio, Kanji
; TITLE OF INVENTION: No. US20030208045Ael Protein and Method for Producing
the Protein
; FILE REFERENCE: FJN-070
; CURRENT APPLICATION NUMBER: US/10/460,623
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: JP 97808/1997
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: JP 151434/1997
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: JP 217897/1997
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: JP 224803/1997
; PRIOR FILING DATE: 1997-08-21
; PRIOR APPLICATION NUMBER: JP 332241/1997
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-460-623-11

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Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIWNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        |||
Db      301 PDODATYFGAFKVRDID 317

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RESULT 14

US-10-289-456-79

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; Sequence 79, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-289-456-79
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Query Match 100.0%; Score 1685; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        |||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 15

US-10-202-062-22

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; Sequence 22, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 317
; TYPE: PRT
; ORGANISM: human

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US-10-202-062-22

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Query Match      100.0%; Score 1685; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Qy      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        |||

```

Db 301 PDQDATYFGAFKVRDID 317

Search completed: April 25, 2005, 14:45:19
Job time : 141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 14:26:55 ; Search time 175 Seconds
(without alignments)
927.595 Million cell updates/sec

Title: US-09-211-315-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
		Query						
Result	No.	Score	Match	Length	DB	ID	Description	
	1	1685	100.0	317	1	TN11_HUMAN	O14788 h tumor nec	
	2	1417.5	84.1	316	1	TN11_MOUSE	O35235 m tumor nec	
	3	1396.5	82.9	318	1	TN11_RAT	Q9ese2 r tumor nec	
	4	266	15.8	317	2	Q7ZYX9	Q7zyx9 brachydanio	
	5	265	15.7	304	2	Q7T1F2	Q7t1f2 gallus gall	
	6	251.5	14.9	281	1	TN10_HUMAN	P50591 homo sapien	
	7	249.5	14.8	299	2	Q6DHG9	Q6dhg9 brachydanio	
	8	248	14.7	291	1	TN10_MOUSE	P50592 mus musculu	
	9	240.5	14.3	214	2	Q9DDZ5	Q9ddz5 brachydanio	
	10	216.5	12.8	287	2	Q90WT9	Q90wt9 gallus gall	
	11	215.5	12.8	287	2	Q8K3G0	Q8k3g0 rattus norv	
	12	200	11.9	282	1	TNF6_PIG	Q9bea8 sus scrofa	
	13	194.5	11.5	280	2	Q861W5	Q861w5 felis silve	
	14	189	11.2	281	1	TNF6_HUMAN	P48023 homo sapien	
	15	187.5	11.1	279	2	Q7TMV9	Q7tmv9 mus musculu	

16	186	11.0	280	1	TNF6_MACFA	P63308	macaca fasc
17	186	11.0	280	1	TNF6_MACMU	P63307	macaca mula
18	186	11.0	280	1	TNF6_MACNE	P63306	macaca neme
19	184.5	10.9	252	2	Q8K3Y8	Q8k3y8	mus musculu
20	184.5	10.9	279	1	TNF6_MOUSE	P41047	mus musculu
21	182.5	10.8	280	1	TNF6_CERTO	Q9bdn1	cercocobus
22	181	10.7	95	2	Q6UWL7	Q6uwl7	homo sapien
23	181	10.7	95	2	Q6UY13	Q6uy13	homo sapien
24	179.5	10.7	252	2	Q80YZ0	Q80yz0	mus musculu
25	177.5	10.5	252	2	Q8K3Y7	Q8k3y7	rattus norv
26	176.5	10.5	261	1	TNF5_BOVIN	P51749	bos taurus
27	175.5	10.4	278	1	TNF6_RAT	P36940	rattus norv
28	169.5	10.1	261	1	TNF5_CALJA	Q9bdn3	callithrix
29	167.5	9.9	261	1	TNF5_AOTTR	Q9bdm3	aotus trivi
30	158.5	9.4	261	1	TNF5_HUMAN	P29965	homo sapien
31	156.5	9.3	251	2	Q8NFE9	Q8nfe9	homo sapien
32	155.5	9.2	261	1	TNF5_CERTO	P63305	cercocobus
33	155.5	9.2	261	1	TNF5_MACMU	P63304	macaca mula
34	155	9.2	272	1	TNF5_CHICK	Q9i8d8	gallus gall
35	152.5	9.1	261	1	TNF5_PIG	Q95mq5	sus scrofa
36	152	9.0	260	1	TNF5_FELCA	O97605	felis silve
37	146	8.7	234	1	TNFA_CAVPO	P51435	cavia porce
38	145.5	8.6	239	1	TN14_MOUSE	Q9qyh9	mus musculu
39	145	8.6	174	1	TN15_HUMAN	O95150	homo sapien
40	145	8.6	260	1	TNF5_CANFA	O97626	canis famil
41	143	8.5	240	1	TNF5_MACNE	Q9bdm7	macaca neme
42	141.5	8.4	235	1	TNFA_MOUSE	P06804	mus musculu
43	140.5	8.3	235	1	TNFA_RABIT	P04924	oryctolagus
44	139.5	8.3	215	2	Q99ND1	Q99nd1	sciurus vul
45	139	8.2	233	1	TNFA_SAISC	Q8mkq8	saimiri sci

ALIGNMENTS

RESULT 1

TN11_HUMAN

ID TN11_HUMAN STANDARD; PRT; 317 AA.
AC O14788; O14723; Q96Q17; Q9P2Q3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANSE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
GN Name=TNFSF11; Synonyms=OPGL, RANKL, TRANSE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow, and Peripheral blood;
RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,

RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph node;
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Ikeda T., Kuroyama H., Hirokawa K.;
 RT "Determination of human RANKL isoforms.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes;
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Tongue;
 RX MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
 RA Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast
 RT formation.";
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SODF;

```

CC      IsoId=O14788-2; Sequence=VSP_006447;
CC      Name=3;
CC      IsoId=O14788-3; Sequence=VSP_006446;
CC      -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC          spleen, peripheral blood Leukocytes, bone marrow, heart, placenta,
CC          skeletal muscle, stomach and thyroid.
CC      -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC      -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC          by proteolytic processing (By similarity). The cleavage may be
CC          catalyzed by ADAM17.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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CC      -----
DR      EMBL; AF019047; AAB86811.1; -.
DR      EMBL; AF053712; AAC39731.1; -.
DR      EMBL; AB064269; BAB79694.1; -.
DR      EMBL; AB061227; BAB71768.1; -.
DR      EMBL; AB064270; BAB79695.1; -.
DR      EMBL; AF013171; AAC51762.1; -.
DR      EMBL; AB037599; BAA90488.1; -.
DR      HSSP; O35235; 1JTZ.
DR      Genew; HGNC:11926; TNFSF11.
DR      MIM; 602642; -.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0005887; C:integral to plasma membrane; NAS.
DR      GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      GO; GO:0030316; P:osteoclast differentiation; NAS.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Alternative splicing; Cytokine; Differentiation; Glycoprotein;
KW      Receptor; Signal-anchor; Transmembrane.
FT      CHAIN      1      317      Tumor necrosis factor ligand superfamily
FT                                     member 11, membrane form.
FT      CHAIN      140     317      Tumor necrosis factor ligand superfamily
FT                                     member 11, soluble form (By similarity).
FT      DOMAIN      1      47      Cytoplasmic (Potential).
FT      TRANSMEM     48      68      Signal-anchor for type II membrane
FT                                     protein (Potential).
FT      DOMAIN      69     317      Extracellular (Potential).
FT      SITE       139     140      Cleavage (By similarity).
FT      CARBOHYD     171     171      N-linked (GlcNAc . .) (Potential).
FT      CARBOHYD     198     198      N-linked (GlcNAc . .) (Potential).
FT      VARSPLIC      1      47      Missing (in isoform 3).

```

FT /FTId=VSP_006446.
 FT VARSPLIC 1 73 Missing (in isoform 2).
 FT /FTId=VSP_006447.
 FT CONFLICT 194 194 A -> G (in Ref. 4).
 SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 100.0%; Score 1685; DB 1; Length 317;
 Best Local Similarity 100.0%; Pred. No. 5.1e-136;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 |||||
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
 |||||
 Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
 |||||
 Db 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
 |||||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

TN11_MOUSE

ID TN11_MOUSE STANDARD; PRT; 316 AA.
 AC O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 DE (OCIF).
 GN Name=Tnfsf11; Synonyms=OPGL, RANKL, Trance;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma;
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,

RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow;
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma;
 RX MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
 RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RT to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.

RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family
 RT member involved in osteoclastogenesis and dendritic cell survival.";
 RL J. Biol. Chem. 274:13613-13618(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RX MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
 CC but not in nonlymphoid tissues and is abundantly expressed in T
 CC cells but not in B cells. A high level expression is also seen in
 CC the trabecular bone and lung.
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
 CC alveolar mammary structures during pregnancy, resulting in death
 CC of newborns. Trance-deficient mice show severe osteopetrosis, with
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit
 CC profound growth retardation at several skeletal sites, including
 CC the limbs, skull, and vertebrae and have marked chondrodysplasia,
 CC with thick, irregular growth plates and a relative increase in
 CC hypertrophic chondrocytes.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

```

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CC -----
DR EMBL; AF013170; AAC71061.1; -.
DR EMBL; AF019048; AAB86812.1; -.
DR EMBL; AF053713; AAC40113.1; -.
DR EMBL; AB008426; BAA25425.1; -.
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR EMBL; AB032771; BAA97257.1; -.
DR EMBL; AB032772; BAA97258.1; -.
DR EMBL; AB036798; BAA97259.1; -.
DR PDB; 1IQA; X-ray; A/B/C=157-316.
DR PDB; 1JTZ; X-ray; X/Y/Z=146-316.
DR MGD; MGI:1100089; Tnfsf11.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042804; F:protein homooligomerization activity; IDA.
DR GO; GO:0045453; P:bone resorption; IDA.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0001503; P:ossification; IMP.
DR GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW 3D-structure; Alternative splicing; Cytokine; Differentiation;
KW Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;
KW Transmembrane.
FT CHAIN 1 316 Tumor necrosis factor ligand superfamily
FT member 11, membrane form.
FT CHAIN 139 316 Tumor necrosis factor ligand superfamily
FT member 11, soluble form.
FT DOMAIN 1 48 Cytoplasmic (Potential).
FT TRANSMEM 49 69 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 70 316 Extracellular (Potential).
FT SITE 138 139 Cleavage.
FT CARBOHYD 197 197 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 262 262 N-linked (GlcNAc . .) (Potential).
FT VARSPLIC 1 117 Missing (in isoform 3).
FT /FTId=VSP_006448.
FT VARSPLIC 14 44 SSEEMSGSGPVPHEGPLHPAPSAPAPAPPPA -> TP (in
FT isoform 2).
FT /FTId=VSP_006449.
FT CONFLICT 99 99 G -> D (in Ref. 2).

```


FT	CONFLICT	141	143	Missing (in Ref. 5).
FT	STRAND	164	169	
FT	TURN	171	172	
FT	STRAND	181	182	
FT	STRAND	186	187	
FT	TURN	191	192	
FT	STRAND	194	196	
FT	STRAND	198	201	
FT	TURN	202	203	

Query Match 84.1%; Score 1417.5; DB 1; Length 316;
 Best Local Similarity 84.3%; Pred. No. 4.4e-113;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQ	59
		:	
Db	1	MRRASRDYGKYLRSEEMSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ	60
Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
		: : : : :	
Db	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRI	118
Qy	120	KQAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS	179
		: :	
Db	119	KQAFQGA VQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHTINAASIPSGS	178
Qy	180	HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
		: : :	
Db	179	HKVTLSSWYHDRGWAKISNMTLSNGKLVRNQDGFYYLYANICFRHHETSGSVPTDYLQLM	238
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLL	299
		: :	
Db	239	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGFFKLRAGEEISIQVSNPSLL	298
Qy	300	DPDQDATYFGAFKVRDID	317
		:	
Db	299	DPDQDATYFGAFKVQDID	316

RESULT 3

TN11_RAT

ID TN11_RAT STANDARD; PRT; 318 AA.

AC Q9ESE2; Q91ZI9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF).

GN Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tibial bone;
 RX MEDLINE=20540945; PubMed=11092398;
 RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
 RA Zheng M.H.;
 RT "Cloning, sequence and functional characterization of the rat
 RT homologue of receptor activator of NF-kB ligand.";
 RL J. Bone Miner. Res. 15:2178-2186(2000).
 RN [2]
 RP SEQUENCE OF 266-318 FROM N.A.
 RC STRAIN=Fischer 344;
 RX MEDLINE=21662371; PubMed=11804028;
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
 RA Marks S.C. Jr.;
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
 RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
 RL Int. J. Dev. Biol. 45:853-859(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF187319; AAG17031.1; -.
 DR EMBL; AF425669; AAL23963.1; -.
 DR HSSP; O35235; 1JTZ.
 DR RGD; 620784; Tnfsf11.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
 KW Transmembrane.
 FT CHAIN 1 318 Tumor necrosis factor ligand superfamily
 FT member 11, membrane form.

FT CHAIN 141 318 Tumor necrosis factor ligand superfamily
 FT member 11, soluble form.
 FT DOMAIN 1 47 Cytoplasmic (Potential).
 FT TRANSMEM 48 68 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 69 318 Extracellular (Potential).
 FT SITE 140 141 Cleavage (By similarity).
 FT CARBOHYD 199 199 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 264 264 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 317 317 I -> M (in Ref. 2).
 SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 82.9%; Score 1396.5; DB 1; Length 318;
 Best Local Similarity 82.4%; Pred. No. 2.8e-111;
 Matches 262; Conservative 19; Mismatches 36; Indels 1; Gaps 1;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQ 59
 ||||:||||| ||| ||||| || ||| ||||| ||:|||||||
 Db 1 MRRANRDYGKYLKGSEEMGSCPGVPHEGPLHPAPSAPAPAPPPAASRFMFLALLGLGLGQ 60
 Qy 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
 ||||:||||| ||||| ||||| || ||| ||||| ||:||||: ||: |||||:
 Db 61 VVCSIALFLYFRAQMDPNRISEDSTRCFYRILRLRENTGLQDSTLESEDTEALPDSCRMM 120
 Qy 120 KQAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGS 179
 ||||| |||||:||||| || |||:|||||:|:| ||||| ||||| |||||
 Db 121 KQAFQGA VQRELQHIVGPQRFSGV PAMMEGSWLDVARRGKPEAQPF AHLTINAADIPSGS 180
 Qy 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
 Db 181 HKVSLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSV PADYLQLM 240
 Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLL 299
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||:|||||: |||||
 Db 241 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVG GFFKL RAGEEISVQVSNPSLL 300
 Qy 300 DPDQDATYFGAFKVRDID 317
 ||||| ||||| |||||:||||
 Db 301 DPDQDATYFGAFKVQDID 318

RESULT 4

Q7ZYX9

ID Q7ZYX9 PRELIMINARY; PRT; 317 AA.

AC Q7ZYX9;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Tnfsf101 protein.

GN Name=tnfsf101;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC044336; AAH44336.1; -.
DR HSSP; P50591; 1D2Q.
DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 15.8%; Score 266; DB 2; Length 317;
Best Local Similarity 26.6%; Pred. No. 2.4e-14;
Matches 79; Conservative 66; Mismatches 122; Indels 30; Gaps 9;

Qy 42 PAASR-----SMFVALLGLGLG--QVVCVALFFYFRAQMDPNRISEDGTHCIYRILRL 93
|| || ::||: : : |: : || | | :: | ||
Db 24 PANSRGRDSPSKLWIAMVVIVVVVLQIASTTGLFVYL--NMSLSQVKSQGVTEELRCLGL 81
Qy 94 HENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRAEKAMVDGSWLD 153
| :| : :| :| : : : :| |: | :| :
Db 82 -LNVLGKDQDIPEDLAQLFGPECMKLAEGIKAYISKVTDISIISKQTLHAARTRTHSYNTT 140
Qy 154 LAK-RSKLEAQPFHAHLTINATDIPS-----GSHKVSLSWYHDRGWAKISN 198
:| : : :| |||::: | | : : :| :| :|
Db 141 GSKFMTTVMQRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLN 200

Qy 199 MTFNSNGKLIVNQDGFYYLYANICFRHHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLM 256
 || :||:| | ||| ||||: : ||: | | :: ||: : ||| | | :
 Db 201 MTLTNGRLRVPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQ--LL 258

Qy 257 KGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
 || || |: :||: :||: || |:|:|:|: : |:|:|: : : :|||:|:|:
 Db 259 KGVGTCWAPDAEYALHSVYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 315

RESULT 5

Q7T1F2

ID Q7T1F2 PRELIMINARY; PRT; 304 AA.
 AC Q7T1F2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Tumor necrosis factor related apoptosis inducing ligand.
 GN Name=TRAIL;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
 RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis
 RT Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
 RT Inducing Ligand (TRAIL).";
 RL J. Vet. Med. Sci. 66:643-650(2004).
 DR EMBL; AB114678; BAC79267.1; -.
 DR HSSP; P50591; 1D2Q.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 15.7%; Score 265; DB 2; Length 304;
 Best Local Similarity 27.3%; Pred. No. 2.8e-14;
 Matches 82; Conservative 56; Mismatches 126; Indels 36; Gaps 12;

Qy 38 PHQPPAASRSMFVALLGLGLGQVVCVVALFFYFRAQMDP--NRISEDGTHCI--YRILRL 93
 | | : : : | : | | | : | | : : | | | : : |
 Db 3 PAGGPPAHTCGAVLVAAVLLQSVCAVVTYIYFTNELKQLWDTYRSRGTACLTGEELGDL 62

Qy 94 HENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRAEKAMVDGSWLD 153
 : | | : ||:| : | | :|| :|| : | : : : ||:

Db 63 IQNLD----VVESKDR--VADPCWQVKWHLGKLIKMMMSRI-----LQENMSAINGDRTQ 111

Qy 154 -LAKRSKLEAQP----FAHLTINATDIPSGSHKV-----SLSSWYHD-RGWAKISNM 199
 |:| : | ||| :: : | : || || : : |:

Db 112 ALSRRDEPPQGPTLRIAHLTGSSKRSSASPHNYLSYRGIGHKIHWSERRGHSFLYNV 171

Qy 200 TFSNGKLIVNQDGFYYLYANICFRHHET----SG--DLATEYLQLMVYVTKTSIKIPSSH 253
 ||:|:| | |||:|: || | || : ||: |:| : |

Db 172 ELWNGELVVPQTGFYYIYSQTYFRFRENEDEDSGLLERIKNPKQLVQYIYKLT-NYPDPI 230

Qy 254 TLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
 ||| | || :|: ||: || |:|: : | : ||| :| |:|:| ||| :

Db 231 LLMKSARTSCWSKKAEGLYSVYQGGVFQLKREDRIFVSVSNSDIVMDKEASFFGAFMI 290

RESULT 6

TN10_HUMAN

ID TN10_HUMAN STANDARD; PRT; 281 AA.

AC P50591;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).

GN Name=TNFSF10; Synonyms=APO2L, TRAIL;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;

RT "Identification and characterization of a new member of the TNF family
 RT that induces apoptosis.";

RL Immunity 3:673-682(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
 RA Ashkenazi A.;

RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
 RT necrosis factor cytokine family.";

RL J. Biol. Chem. 271:12687-12690(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed=10542098; DOI=10.1038/14935;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Screaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
RA Sung Y.C., Oh B.-H.;
RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
RT selective antitumor activity.";
RL Immunity 11:253-261(1999).

CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.

CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
CC trimer.

CC -!- SUBUNIT: Homotrimer.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
CC and prostate.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U37518; AAC50332.1; -.
DR EMBL; U57059; AAB01233.1; -.
DR EMBL; BC032722; AAH32722.1; -.
DR PDB; 1D0G; X-ray; A/B/D=114-281.
DR PDB; 1D2Q; X-ray; A=114-281.
DR PDB; 1D4V; X-ray; B=119-281.
DR PDB; 1DG6; X-ray; A=91-281.
DR PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.
DR Genew; HGNC:11925; TNFSF10.
DR H-InvDB; HIX0003863; -.
DR MIM; 603598; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;
KW Transmembrane; Zinc.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 39 281 Extracellular (Potential).
FT METAL 230 230 Zinc.
FT STRAND 123 127
FT STRAND 149 150
FT STRAND 163 165
FT STRAND 167 170
FT TURN 171 172
FT STRAND 173 176
FT STRAND 180 193
FT TURN 198 199
FT STRAND 205 213
FT STRAND 220 228
FT TURN 233 234
FT STRAND 237 250
FT TURN 252 253
FT STRAND 255 260
FT HELIX 263 265
FT STRAND 266 267
FT TURN 270 272
FT STRAND 274 279
SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match

14.9%; Score 251.5; DB 1; Length 281;

Best Local Similarity 24.1%; Pred. No. 3.6e-13;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

```

Qy      42 PAASRSMFVALLGLGLGQVVCVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF 99
      |: :: : :: | | : | : | : | : | : | : | :
Db      10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKED--- 61

Qy     100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
      |: : | : : | ::| :|: :| :| : : : :
Db      62 -DSYWDPNDEESMNSPCWQVKW-----QLRQLVRKMILRTSEETI-----STVQEKQ 107

Qy     160 LEAQPF-----AHLT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199
      | : : : | :| : | : : :| :| :| : :| :
Db     108 QNISPLVRERGPQ RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167

Qy     200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
      ||:|::: |||:|: || | : |:: |: | : | ||
Db     168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy     260 STKYWSGNSEFHFYSINVGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
      || ::|: ||| || |:|: : | : |:| |:| :|::| || |
Db     227 RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

```

RESULT 7

Q6DHG9

```

ID   Q6DHG9          PRELIMINARY;          PRT;    299 AA.
AC   Q6DHG9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Zgc:92320.
GN   Name=zgc:92320;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

```

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC076005; AAH76005.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 14.8%; Score 249.5; DB 2; Length 299;
 Best Local Similarity 28.1%; Pred. No. 5.8e-13;
 Matches 85; Conservative 49; Mismatches 126; Indels 43; Gaps 13;

Qy 44 ASRSM-FVALLGLG--LGQVVCVALFFYFRAQMDPNR--ISEDGTHCIYRI-LRLHENA 97
 :| :| ::|| | | : | | : : | : | | :
 Db 6 SSHTMQYIGLLLLLAAILLQTIHAVTFIYFSNVLSTMKETFSKSSVSCLMRANLRTIKGQ 65
 Qy 98 DFQDTTLESQDTKLIPDSCRRIKQ-----AFQGAVQKELQHIVGSQHIRAEKAMVDG 149
 : | :| | | :: | : | | : | : | :|
 Db 66 ELNGA--EGKD-----DPCWQVTQQLHFLIEKSMSSRYQKEITSAVKDEVSRVLP SLVIQ 118
 Qy 150 SWLDLAKRSKLEAQPF AHLTINATDIPSG--SHKV---SLSSWYHDRGWAKISNMTFSNG 204
 | : | | : | | : : | : | | : | | : | :|
 Db 119 DQED-SSRPKIAAHVTG SYTPESKDGAGLPNRKVYGGKIQSWESEKGLAFLQ NVELSDG 177
 Qy 205 KLIVNQDGFYYLYANICFRH---HETSGDLATEY-----LQLMVYVTKTSIKIP 250
 :| :| | | | :| :| | | | | : | | :| :| :|
 Db 178 ELVVPQAGLYYIYSQTYFRHTLIEEDESAREDEY GSMGESVRGK PMLQYVYKKVSSYQVP 237
 Qy 251 SSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQDATYFGA 310
 ||| | | :|| : || | | :| | : : : ||| | :| | : :|||
 Db 238 I--LLMKNARTTCWSRDSEYGLYSIQAGLFQLGSGDRV FVTVSNVSTIDMDEKSSFFGA 295
 Qy 311 FKV 313
 | |
 Db 296 FLV 298

RESULT 8

TN10_MOUSE

ID TN10_MOUSE STANDARD; PRT; 291 AA.

AC P50592;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN Name=Tnfsf10; Synonyms=Trail;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF family
 RT that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Widespread.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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 CC or send an email to license@isb-sib.ch).

 DR EMBL; U37522; AAC52345.1; -.
 DR HSSP; P50591; 1D2Q.
 DR MGD; MGI:107414; Tnfsf10.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.
 FT DOMAIN 1 17 Cytoplasmic (Potential).
 FT TRANSMEM 18 38 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 39 291 Extracellular (Potential).
 FT CARBOHYD 52 52 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.7%; Score 248; DB 1; Length 291;
 Best Local Similarity 25.4%; Pred. No. 7.6e-13;
 Matches 79; Conservative 52; Mismatches 100; Indels 80; Gaps 13;

```

Qy      46 RSMFVALLGLG-LGQVVC SVALFFYFRAQMD--PNRI SEDGTHCIYRILRLHENADFQDT 102
      | | : :: | | | : | | : | : | | : : | | :
Db      17 RMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-----TDEDFWDS 71

Qy     103 TLESQDTKLIPDSCRRIK-----QAFQ-----GAVQKEL 131
      |   | :: | :: | : | |   | |
Db      72 T----DGEILNRPC LQV KRQLYQLIEEVT LRTFQDTISTVPEKQLSTPPLPRGGR PQKVA 127

Qy     132 QHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLS SWYHDR 191
      | | |   | : | : : : | | |   | : | | |
Db     128 AHITGITR-RSNSALI-----PISKDGKTLGQ-----KIESWESSR 162

Qy     192 -GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL-----QLMVYV 242
      | : :: : | | | : : | | | : | | |   | : : : | | :
Db     163 KGHSFLNHVLF R NGELVIEQEGLYYIYSQTYFRFQEAED--ASKMVSKDKVRTKQLVQYI 220

Qy     243 TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLDPD 302
      | : |   | | |   | | : : : | | | | | : : : | : | : |
Db     221 YKYT-SYPDPIVLMKSARN SCWSRDAEYGLYSIQGGLFELKKNDRIFVSVTNEHLM DLD 279

Qy     303 QDATYFGAFKV 313
      | : : : | | | :
Db     280 QEASFFGAFLI 290
  
```

RESULT 9

Q9DDZ5

```

ID   Q9DDZ5          PRELIMINARY;          PRT;          214 AA.
AC   Q9DDZ5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   TRAIL-like protein.
GN   Name=tnfsf101;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bobe J., Goetz F.W.;
RT   "Molecular cloning and expression of a TNF receptor and two TNF
RT   ligands in the fish ovary.";
RL   Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR   EMBL; AF250041; AAG47640.1; -.
DR   HSSP; P50591; 1D2Q.
DR   ZFIN; ZDB-GENE-010801-1; tnfsf101.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
  
```

DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 14.3%; Score 240.5; DB 2; Length 214;
Best Local Similarity 28.6%; Pred. No. 2.2e-12;
Matches 61; Conservative 50; Mismatches 83; Indels 19; Gaps 5;

Qy 118 RIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAK-RSKLEAQPF AHLTINATDIP 176
:: : : : | : | : | : : | : : : | |||:::
Db 2 KLAEGIKAYISKV TDSIISKQTLHAARTQTHSYNTTGSKFMTTVMQRPSAHLTLSSASDN 61
Qy 177 S-----GSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICF 222
| : : : | : | : || : || : || : || : : |
Db 62 SRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLNMTLTNGRLRVPQDGRYYLYSQVYF 121
Qy 223 RHHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280
| : | | : : || : : || | : || | | : : : : : : ||
Db 122 RYPSPSDSQSSVSHQLVQCIYKKTSYLNPIQ--LLKGVGTCWAPDAEYALHSVYQGGGL 179
Qy 281 FKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
| : || : || : : || : || : : : : ||| : :
Db 180 FELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212

RESULT 10

Q90WT9

ID Q90WT9 PRELIMINARY; PRT; 287 AA.
AC Q90WT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand-like protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY057941; AAL23702.1; -.
DR HSSP; P50591; 1D2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 12.8%; Score 216.5; DB 2; Length 287;
 Best Local Similarity 24.7%; Pred. No. 3.7e-10;
 Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;

```

Qy      80 SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQH 139
      | : | : | : | : : : : : : : : : : : : : : : : : : : : : : :
Db      51 SSEELRCLQLINQQQEGSNLEEL-----ISNQSCLKLANTIKAYVATVTENVISRSV 102

Qy     140 I-RAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIP-----SGSHKVSLSW 187
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     103 VNEAQKSYFNISEGQVA--TKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW 160

Qy     188 YHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVT-KTS 246
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     161 EDSTIHSHLQNITYRDGRLRVNQAGKYVYSQIYFRYSRDGAGARVSVPLVQCINWKTS 220

Qy     247 IKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSCEEISIEVSNPSLLDPDQDAT 306
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     221 YSQPI--LLLKGVGTCWAPEAEYGLHALYQGGLFELKAGDELFSVSVSLAIDYSDAAS 278

Qy     307 YFGAFKV 313
      ||||| :
Db     279 YFGAFRL 285
  
```

RESULT 11

Q8K3G0

```

ID   Q8K3G0          PRELIMINARY;          PRT;    287 AA.
AC   Q8K3G0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   TNF-related apoptosis inducing ligand.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DA;
RA   Mueller A.M., Giegerich G.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY115578; AAM49797.1; -.
DR   HSSP; P50591; 1D2Q.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE    287 AA;  32979 MW;  CA4F5B5D7C833FEC CRC64;
  
```

Query Match 12.8%; Score 215.5; DB 2; Length 287;
 Best Local Similarity 24.2%; Pred. No. 4.5e-10;
 Matches 73; Conservative 59; Mismatches 113; Indels 57; Gaps 14;

```

Qy      42 PAASRSMFVALLGLGLGQVV---CSVAL-FFYFRAQMD--PNRISEDGTHCIYRILRLHE 95
      |: |:  : :: : | |:  : |: : || : :  : |: | | :  |
Db      10 PSFSQHFTMTVICIVLLQVLLQALTVAVTYMYFNNEVKQLQDNYSKIGLACFSK-----E 64

Qy      96 NADFQDTTLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRA-EKAMVDGSWLDL 154
      : || |:|  | ::  | ::|  ::| ::  :| ||  :
Db      65 DGDFWDST----DEGILNRPCQLQVK-----RQLYQLIEEVTLRTFEKT-----IST 106

Qy     155 AKRSKLEAQPFI-----AHLT-----INATDIPSGSHKVSL----SSWYHD-RGWA 194
      :|  |  ||:|  |  ||  :|  :|  || :
Db     107 VPEKQLSTPPLPRGRRPQRVAAHITGITRRSNLALIPISKDGKTLGQKIETWESSRRGHS 166

Qy     195 KISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLAT-----EYLQLMVYVTKTSIK 248
      ::::  ||:|:: ::| ||:|:  :|  |  |  |:: |:: | :
Db     167 FLNHVHLRNGELVIOEEGLYYIYSQTYRFEAKEASKTVSKDGGRIKQMVQYIYKYT-S 225

Qy     249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSGEEISIEVSNPSLLDPDQDATYF 308
      |  |||  || :|: ||| || |:|:  :| : |:| |:| |::|
Db     226 YPDPIILLMKSARNSCWSREAEGLYSIYQGGLFELKENDRIFVSVTNEHLMDLDHEASFF 285

Qy     309 GA 310
      ||
Db     286 GA 287
  
```

RESULT 12

TNF6_PIG

```

ID  TNF6_PIG          STANDARD;          PRT;   282 AA.
AC  Q9BEA8; Q95M04; Q95N10;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE  ligand).
GN  Name=TNFSF6; Synonyms=FASL;
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21322533; PubMed=11429161; DOI=10.1089/107999001300177493;
RA  Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT  "Molecular cloning, characterization, and expression of porcine Fas
RT  ligand (CD95 ligand).";
RL  J. Interferon Cytokine Res. 21:305-312(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Guanxi bama miniature pig;
RA  Zhu N., Young Y.;
RT  "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL  Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN  [3]
  
```

RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 RA Tsuyuki S., Kono M., Bloom E.T.;
 RT "Cloning and potential utility of porcine Fas ligand: overexpression
 RT in porcine cells protects them from attack by human cytolytic cells.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;
 RX MEDLINE=21653191; PubMed=11792426; DOI=10.1016/S0161-5890(01)00098-0;
 RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
 RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison
 RT with human gene.";
 RL Mol. Immunol. 38:581-586(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
 CC modulates its effects (By similarity).
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- INDUCTION: By IL-18.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB027297; BAB40919.1; -.
 DR EMBL; AY033634; AAK56449.1; -.
 DR EMBL; AF397407; AAK84408.1; -.
 DR EMBL; AB069764; BAB64291.1; -.
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR008064; Fas_ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01681; FASLIGAND.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
 FT CHAIN 1 282 Tumor necrosis factor ligand superfamily
 FT member 6, membrane form.

FT	CHAIN	131	282	Tumor necrosis factor ligand superfamily
FT				member 6, soluble form (By similarity).
FT	DOMAIN	1	82	Cytoplasmic (Potential).
FT	TRANSMEM	83	103	Signal-anchor for type II membrane
FT				protein (Potential).
FT	DOMAIN	104	282	Extracellular (Potential).
FT	DOMAIN	4	70	Pro-rich.
FT	DOMAIN	45	56	Poly-Pro.
FT	SITE	130	131	Cleavage (By similarity).
FT	DISULFID	203	234	Potential.
FT	CARBOHYD	185	185	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	251	251	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	261	261	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	5	5	F -> L (in Ref. 4).
FT	CONFLICT	57	57	T -> P (in Ref. 2).
SQ	SEQUENCE	282 AA;	31756 MW;	6743DAA1145671FB CRC64;

Query Match 11.9%; Score 200; DB 1; Length 282;
 Best Local Similarity 23.0%; Pred. No. 9.5e-09;
 Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

Qy	22	PGAPHEGPLHAPPPPAPHQPPAA---SRSM-----FVA	51
		:	
Db	37	PGRP--GQRRPPPPPPPPPTLLPSRPLPPLPPPSLKKKRDHNAGLCLLMFFMVLVA	94
Qy	52	LLGLGLGQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKL	111
		: : : : : :	
Db	95	LVGLGLG-----MFQLFHLQKE-----LTELRRESASQRHT-----	124
Qy	112	IPDSCRRIKQAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLT--	169
		: : : : : :	
Db	125	-----ESSLEKQIGHPNLPSEKK-----ELRKVAHLTGK	153
Qy	170	INATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSG	229
		: : : : : : : :	
Db	154	PNSRSIP-----LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCN-	204
Qy	230	DLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFCKL	283
		: : : : : : :	
Db	205	---NQPLSHKVY-TRNS-RYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGAVFNL	252
Qy	284	RSGEEISIEVSNPSLLDPDQDATYFGAFKV	313
		: : : : : : : : :	
Db	253	TSADHLYVNVSELSLVNFEEKSTFFGLYKL	282

RESULT 13

Q861W5

ID Q861W5 PRELIMINARY; PRT; 280 AA.

AC Q861W5;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Fas ligand.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99053606; PubMed=9839871; DOI=10.1016/S0165-2427(98)00151-2;
 RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,
 RA Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs."
 RL Vet. Immunol. Immunopathol. 65:161-172(1998).
 DR EMBL; AB009280; BAC76426.1; -.
 DR HSSP; P01374; 1TNR.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR008064; Fas_ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01681; FASLIGAND.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 280 AA; 31361 MW; 6AA7E2DE1F1A6B5C CRC64;

Query Match 11.5%; Score 194.5; DB 2; Length 280;
 Best Local Similarity 22.8%; Pred. No. 2.8e-08;
 Matches 74; Conservative 40; Mismatches 98; Indels 113; Gaps 12;

Qy	20	GGPG----	APHEGPLHAPPPAPHQPPAASRSM-----	FVALLGLG	56
			:		
Db	38	GRPGQRRPPPPPPPTLPPPPPPPPPLPPLPLPPLKTRRDHNTGLCLLVMMFFMVLVALVGLG			97
Qy	57	LGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSC			116
			:	: : : :	
Db	98	LG-----	MFQLFHLQ-----	KELAELESTSQKH-----	121
Qy	117	RIKQAFQGA	VQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLT--	INATD	174
			: : : :	: :	
Db	122	-----	VASSLEKQIGQLNPPSEKR-----	ELRKVAHLTGKPNRSRS	156
Qy	175	IPSGSHKVSLS	SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATE		234
			: : : : : : : : :		
Db	157	IP-----	LEWEDTYGIALVSGVKYKKGGLVINDTGMVFVYSKVNFRGQSCN----	NQ	204
Qy	235	YLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----	WSGNSEFHFYSINVGGFFKLRS	GEE	288
			: : :	: : : :	
Db	205	PLNHKVMYMRNS--	KYPQDLVLMEGKMMNYCTTGQMWARSS-----	YLGAVFNLT	SADH 255
Qy	289	ISIEVSNPSLLDPDQDATYFGAFKV			313
		: :	: : : : :		
Db	256	LYVNVSELSLVSFEESKTFFGLYKL			280

RESULT 14

TNF6_HUMAN

ID TNF6_HUMAN STANDARD; PRT; 281 AA.
AC P48023; Q9BZP9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN Name=TNFSF6; Synonyms=APT1LG1, FASL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
RT specificity.";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Blood;
 RA Matsumura M., Nakanishi Y., Ohba Y.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
 RX MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
 RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
 RA Terskikh A., Peitsch M.C., Tschopp J.;
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction."
 RL J. Biol. Chem. 272:18827-18833(1997).
 RN [10]
 RP PROCESSING.
 RX MEDLINE=98087475; PubMed=9427603;
 RA Tanaka M., Itai T., Adachi M., Nagata S.;
 RT "Downregulation of Fas ligand by shedding."
 RL Nat. Med. 4:31-36(1998).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
 CC modulates its effects.
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
 CC into the extracellular fluid, probably by cleavage from the cell
 CC surface.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P48023-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: The soluble form derives from the membrane form by

CC proteolytic processing.
 CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
 CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
 CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
 CC involving hemolytic anemia and thrombocytopenia with massive
 CC lymphadenopathy and splenomegaly.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".

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 CC -----

DR EMBL; X89102; CAA61474.1; -.
 DR EMBL; U08137; AAC50071.1; -.
 DR EMBL; U11821; AAC50124.1; -.
 DR EMBL; D38122; BAA07320.1; -.
 DR EMBL; AF288573; AAG60017.1; -.
 DR EMBL; Z96050; CAB09424.1; -.
 DR EMBL; BC017502; AAH17502.1; -.
 DR EMBL; AB013303; BAA32542.1; -.
 DR PIR; I38707; I38707.
 DR HSSP; P50591; 1D2Q.
 DR Genew; HGNC:11936; TNFSF6.
 DR H-InvDB; HIX0001337; -.
 DR MIM; 134638; -.
 DR MIM; 601859; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008064; Fas_ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01681; FASLIGAND.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;
 KW Signal-anchor; Transmembrane.
 FT CHAIN 1 281 Tumor necrosis factor ligand superfamily
 FT member 6, membrane form.
 FT CHAIN 130 281 Tumor necrosis factor ligand superfamily
 FT member 6, soluble form.
 FT DOMAIN 1 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 102 Signal-anchor for type II membrane

FT				protein (Potential).
FT	DOMAIN	103	281	Extracellular (Potential).
FT	DOMAIN	4	70	Pro-rich.
FT	DOMAIN	45	65	Poly-Pro.
FT	SITE	129	130	Cleavage.
FT	DISULFID	202	233	Potential.
FT	CARBOHYD	184	184	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	250	250	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	260	260	N-linked (GlcNAc. . .) (Potential).
FT	VARSP LIC	117	127	STSQMHTASSL -> ATPVHPLKKRS (in isoform 2).
FT				/FTId=VSP_006443.
FT	VARSP LIC	128	281	Missing (in isoform 2).
FT				/FTId=VSP_006444.
FT	MUTAGEN	206	206	P->D,F,R: Lowers binding to TNFRSF6 and reduces cytotoxicity more than 100-fold.
FT	MUTAGEN	218	218	Y->F,R: Lowers binding to TNFRSF6 and abolishes cytotoxicity.
FT	MUTAGEN	275	275	F->L: Abolishes binding to TNFRSF6 and cytotoxicity.
SQ	SEQUENCE	281 AA;	31485 MW;	A8A6EB358246E9BB CRC64;

Query Match 11.2%; Score 189; DB 1; Length 281;
 Best Local Similarity 21.7%; Pred. No. 8.3e-08;
 Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

Qy	22	PGAPHEGPLHAPPPPAP----	HQPPAASRS-----	MFVALLGLGLGQVVCS	63
				:	
Db	46	PPPPPPPLPPPPPPPLPPLPLPPLK	RGNHSTGLCLLMFFMV	LVALVGLGLG----	100
Qy	64	VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF			123
		:	: : : :		
Db	101	--MFQLFHLQ-----	KELAE	RESTSQMHTA-----	124
Qy	124	QGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPF	AHLT--	INATDIPSGSHK	181
		: : : : :	:	: :	
Db	125	--SSLEKQIGH-----	PSPPPEKKELRKVAHLT	GKSNSRSMP----	159
Qy	182	VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQ	LMVY		241
		: : : : : : : :	:		
Db	160	---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----	LPLSHK		210
Qy	242	VTKTSIKIPSSHTLMKGGSTKY-----	WSGNSEFHFYSINVG	GFFKLRS	295
		: : :	: :	: : : :	
Db	211	VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----	YLGAVFNLT	SADHLYVNVSE	263
Qy	296	PSLLDPDQDATYFGAFKV			313
		: : : : : : :			
Db	264	LSLVNFEE	SQTFFGLYKL		281

RESULT 15

Q7TMV9

ID	Q7TMV9	PRELIMINARY;	PRT;	279 AA.
AC	Q7TMV9;			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Tnfsf6 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC052866; AAH52866.1; -.
 DR HSSP; P50591; 1DG6.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0046666; P:retinal programmed cell death; IMP.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 279 AA; 31416 MW; C2972E2728FBBB7B CRC64;

Query Match 11.1%; Score 187.5; DB 2; Length 279;
 Best Local Similarity 21.7%; Pred. No. 1.1e-07;
 Matches 70; Conservative 46; Mismatches 105; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPHLAPPPAPHPQ-----PAASRSMFVALLGLGL 57
 || :: | | || | | | | : |||:|:|
 Db 38 RGPDQRRPPPPPPVSPPLPPSQPLPLPLTPLKKKDHNTNLWLPVVFVFMVLVALVGMGL 97

Qy	58	GQVVC	SVALFF	YFRAQ	MDPNRI	SEDGTH	CIYRIL	RLHENAD	FQDTT	LESQDT	KLIPD	SCR	117	
							:	:	:					
Db	98	G	-----MYQLFHL-----										105	
Qy	118	RIKQAF	QGA	VQKEL	QHI	--VGSQ	HIRA	---EKAM	VDG	SWL	DLAKR	SKLEA	QPF	
			:	:	:	:	:	:	:	:	:	:	:	
Db	106	-----QKELAE											150	
Qy	173	TDIPSG	SHKVS	LS-SWY	HDRG	WAKIS	NMTFS	NGKLIV	NQDGF	YYLY	ANICFR	HHETSG	DL	
			:			:	:	:	:	:	:	:	:	
Db	151	-----PHSR											201	
Qy	232	ATEYLQ	LMVYV	TKTSI	KIPSS	HTLMK	GGSTKY	WGSN	SEFHF	YSINV	GGFFK	LRSGEE	ISI	
		:	:	:	:	:	:	:	:	:	:	:	:	
Db	202	-NQPLNHKVYMRNS--KYPEDL											257	
Qy	292	EVS	NPSLL	DPDQ	DATY	FGAF	KV							313
		:	:	:	:	:	:							
Db	258	NISQLSLINFEEKSTFFGLYKL											279	

Search completed: April 25, 2005, 14:32:53
Job time : 182 secs